

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 9, 2006, 00:11:07 ; Search time 96.46 Seconds
 (without alignments)
 61.619 Million cell updates/sec

Title: US-10-797-626-1
 Perfect score: 62
 Sequence: 1 STQNASLLSLTVC 13

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : A_Geneseq_8:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*
- 9: Geneseq2005s:*
- 10: Geneseq2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	62	100.0	13	ADSL18077	Adsl18077 Laminin s
2	43	69.4	18	ADSL18079	Adsl18079 Laminin s
3	43	69.4	18	ADSL18078	Adsl18078 Laminin s
4	42	67.7	702	ADSL29055	Adsl29055 Bacterial
5	39	62.9	333	AGG79751	Agg79751 Truncated
6	39	62.9	466	ADQ76869	Adq76869 Mouse ang
7	39	62.9	469	AAV08690	Aav08690 Murine ge
8	39	62.9	580	AAV08692	Aav08692 Murine ge
9	39	62.9	812	AAV08395	Aav08395 Complete
10	39	62.9	812	AAV07585	Aav07585 Murine pl
11	39	62.9	812	AAV08686	Aav08686 Murine pl
12	39	62.9	812	AAW94036	Aaw94036 Murine pl
13	39	62.9	812	AAW94036	Aaw94036 Murine pl
14	39	62.9	812	AAW94036	Aaw94036 Murine pl
15	39	62.9	812	AAW94036	Aaw94036 Murine pl
16	39	62.9	812	AAW94036	Aaw94036 Murine pl
17	39	62.9	812	AAW94036	Aaw94036 Murine pl
18	39	62.9	812	AAW94036	Aaw94036 Murine pl
19	39	62.9	812	AAW94036	Aaw94036 Murine pl
20	39	62.9	812	AAW94036	Aaw94036 Murine pl
21	39	62.9	812	AAW94036	Aaw94036 Murine pl
22	39	62.9	812	AAW94036	Aaw94036 Murine pl
23	39	62.9	2000	ABR53118	AbR53118 Protein s

24	39	62.9	2000	7	ADK62826	ADK62826 Disease t
25	38	61.3	107	5	ABB89730	ABB89730 Human pol
26	37	59.7	121	3	AAG26056	Aag26056 Zea mays
27	37	59.7	137	3	AAG26055	Aag26055 Zea mays
28	37	59.7	292	7	AAO31107	Aao31107 Human mon
29	37	59.7	292	7	AAO31107	Aao31107 Human mon
30	37	59.7	292	7	AAO31107	Aao31107 Human mon
31	37	59.7	412	8	ADX67385	Adx67385 Plant ful
32	37	59.7	412	8	ADX67385	Adx67385 Plant ful
33	36	58.1	18	4	AAI16551	Aai16551 Peptide #
34	36	58.1	18	4	AAI16551	Aai16551 Peptide #
35	36	58.1	18	4	AAI16551	Aai16551 Peptide #
36	36	58.1	18	4	AAI16551	Aai16551 Peptide #
37	36	58.1	18	4	AAI16551	Aai16551 Peptide #
38	36	58.1	18	4	AAI16551	Aai16551 Peptide #
39	36	58.1	18	4	AAI16551	Aai16551 Peptide #
40	36	58.1	18	4	AAI16551	Aai16551 Peptide #
41	36	58.1	18	4	AAI16551	Aai16551 Peptide #
42	36	58.1	18	4	AAI16551	Aai16551 Peptide #
43	36	58.1	153	9	ABE41816	Aeb41816 L. pneumo
44	36	58.1	166	9	ABE38574	Aeb38574 L. pneumo
45	36	58.1	252	8	ADN20863	Adn20863 Bacterial
46	36	58.1	288	8	ADI62525	Adi62525 Mouse LRH
47	36	58.1	375	6	ABU25997	Abu25997 Protein e
48	36	58.1	560	2	AAI21814	Aai21814 Mouse liv
49	36	58.1	560	8	ADI62533	Adi62533 Mouse LRH
50	36	58.1	560	8	ADI62533	Adi62533 Mouse LRH
51	36	58.1	812	3	AAI50872	Aai50872 Bovine pl
52	36	58.1	812	3	AAI50872	Aai50872 Bovine pl
53	36	58.1	812	4	AAI50872	Aai50872 Bovine pl
54	36	58.1	1313	4	ADL91597	Adl91597 Fission y
55	36	58.1	2015	4	ABE65890	Aeb65890 Drosophil
56	35	56.5	28	3	AAI65042	Aai65042 Human 5'
57	35	56.5	28	8	ADU72606	Adu72606 Signal pe
58	35	56.5	28	9	ADZ73597	Adz73597 Human inc
59	35	56.5	155	4	AAU30130	Aau30130 Novel hum
60	35	56.5	269	4	AAU30131	Aau30131 Novel hum
61	35	56.5	277	7	ADH86273	Adh86273 Enterococ
62	35	56.5	358	7	ABO68039	AbO68039 Pseudomon
63	35	56.5	360	4	ABG22212	Abg22212 Novel hum
64	35	56.5	403	4	AAU34981	Aau34981 Enterococ
65	35	56.5	403	6	ABU14650	Abu14650 Protein e
66	35	56.5	404	4	AAU33427	Aau33427 Enterococ
67	35	56.5	428	5	ABB92485	Abb92485 Herbicida
68	35	56.5	629	4	ABG17779	Abg17779 Novel hum
69	35	56.5	664	6	ABU34784	Abu34784 Protein e
70	35	56.5	667	4	ABG28737	Abg28737 Novel hum
71	34	54.8	20	4	AAH82591	Aah82591 Human pro
72	34	54.8	45	4	AAH82583	Aah82583 Human pro
73	34	54.8	47	3	AAH27175	Aah27175 Sendai vi
74	34	54.8	64	5	ABP64178	Abp64178 Human ORF
75	34	54.8	79	9	ADM69713	Adm69713 D melanog
76	34	54.8	116	8	ADS98039	Ads98039 Protein f
77	34	54.8	143	8	ADQ66363	Adq66363 Novel hum
78	34	54.8	179	6	ABU47487	Abu47487 Protein e
79	34	54.8	179	6	ABU45427	Abu45427 Protein e
80	34	54.8	183	9	ABM93005	Abm93005 M. xanthu
81	34	54.8	211	4	AAU16629	Aau16629 Human nov
82	34	54.8	211	6	ABU55698	Abu55698 Human nov
83	34	54.8	245	8	ADN22319	Adn22319 Bacterial
84	34	54.8	262	5	ABB48921	Abb48921 Listeria
85	34	54.8	262	6	ABU32967	Abu32967 Protein e
86	34	54.8	278	6	ABU25195	Abu25195 Protein e
87	34	54.8	286	8	ADJ25712	Adj25712 Polypepti
88	34	54.8	296	7	ADH87107	Adh87107 Enterococ
89	34	54.8	303	4	ABB68577	Abb68577 Drosophil
90	34	54.8	303	8	ADY96480	Ady96480 Drosophil
91	34	54.8	304	8	ADY22538	Ady22538 Plant ful
92	34	54.8	308	5	AAO14222	Aao14222 C elegans
93	34	54.8	314	7	ABO70854	AbO70854 Pseudomon
94	34	54.8	323	5	ADI28025	Adi28025 ECMCAD pr
95	34	54.8	323	8	ABM84851	Abm84851 Human dia
96	34	54.8	326	4	AAH82590	Aah82590 Human pro

97	34	54.8	326	4	AAU14511	Aau14511 Human nov	170	33	53.2	19	9	ADY38279	Ady38279 Human CPP
98	34	54.8	326	4	AAU14275	Aau14275 Human nov	171	33	53.2	19	10	AEF43226	Aef43226 Human Mui
99	34	54.8	326	10	AEF43227	Aee24185 Novel hum	172	33	53.2	20	10	AEF43227	Aef43227 Human Mui
100	34	54.8	326	10	AEF43227	Aee23713 Novel hum	173	33	53.2	29	2	AAW88566	AAw88566 Secreted
101	34	54.8	326	8	ADH80829	Adh80829 Human pol	174	33	53.2	29	2	AAW88566	AAw88566 Secreted
102	34	54.8	326	5	ADH80829	Adh80829 Human pol	175	33	53.2	29	6	ABO44590	ABO44590 Novel hum
103	34	54.8	326	5	ADH80829	Adh80829 Human pol	176	33	53.2	29	7	ABO44590	ABO44590 Novel hum
104	34	54.8	326	8	ADH80829	Adh80829 Human pol	177	33	53.2	29	7	ABO44590	ABO44590 Novel hum
105	34	54.8	326	8	ADH80829	Adh80829 Human pol	178	33	53.2	40	4	AAU01625	AAu01625 Human sec
106	34	54.8	326	4	AAU01625	AAu01625 Human sec	179	33	53.2	40	4	AAU01625	AAu01625 Human sec
107	34	54.8	326	4	AAU01625	AAu01625 Human sec	180	33	53.2	44	4	AAU01625	AAu01625 Human sec
108	34	54.8	326	5	ABW77546	Abw77546 Human pol	181	33	53.2	44	4	ABW77546	Abw77546 Human pol
109	34	54.8	326	8	ADN05759	Adn05759 Antipicori	182	33	53.2	44	4	ABW77546	Abw77546 Human pol
110	34	54.8	326	8	ADN05759	Adn05759 Antipicori	183	33	53.2	44	4	ABW77546	Abw77546 Human pol
111	34	54.8	326	8	ADN05759	Adn05759 Antipicori	184	33	53.2	44	4	ABW77546	Abw77546 Human pol
112	34	54.8	326	8	ADN05759	Adn05759 Antipicori	185	33	53.2	44	4	ABW77546	Abw77546 Human pol
113	34	54.8	326	8	ADN05759	Adn05759 Antipicori	186	33	53.2	44	4	ABW77546	Abw77546 Human pol
114	34	54.8	326	8	ADN05759	Adn05759 Antipicori	187	33	53.2	44	4	ABW77546	Abw77546 Human pol
115	34	54.8	326	8	ADN05759	Adn05759 Antipicori	188	33	53.2	44	4	ABW77546	Abw77546 Human pol
116	34	54.8	326	8	ADN05759	Adn05759 Antipicori	189	33	53.2	44	4	ABW77546	Abw77546 Human pol
117	34	54.8	326	5	ABP74069	Abp74069 Candida a	190	33	53.2	50	4	AAO04908	AAO04908 Human pol
118	34	54.8	326	4	AAU13694	Aau13694 Arabidops	191	33	53.2	65	10	AEF87491	Aef87491 Glycosyls
119	34	54.8	326	3	AAU13694	Aau13694 Arabidops	192	33	53.2	71	2	AAW88640	AAw88640 Secreted
120	34	54.8	326	3	AAU13694	Aau13694 Arabidops	193	33	53.2	71	2	AAW88640	AAw88640 Secreted
121	34	54.8	326	3	AAU13694	Aau13694 Arabidops	194	33	53.2	71	4	ABO44664	ABO44664 Novel hum
122	34	54.8	326	4	AAU13694	Aau13694 Arabidops	195	33	53.2	71	6	ABO44664	ABO44664 Novel hum
123	34	54.8	326	4	AAU13694	Aau13694 Arabidops	196	33	53.2	71	7	ABO44664	ABO44664 Novel hum
124	34	54.8	326	4	AAU13694	Aau13694 Arabidops	197	33	53.2	73	6	ABM47854	ABM47854 Propionib
125	34	54.8	326	4	AAU13694	Aau13694 Arabidops	198	33	53.2	73	6	ABM47854	ABM47854 Propionib
126	34	54.8	326	4	AAU13694	Aau13694 Arabidops	199	33	53.2	76	6	ABM40223	ABM40223 Propionib
127	34	54.8	326	4	AAU13694	Aau13694 Arabidops	200	33	53.2	76	6	ABM40223	ABM40223 Propionib
128	34	54.8	326	4	AAU13694	Aau13694 Arabidops	201	33	53.2	77	3	AAU22815	AAU22815 Human pla
129	34	54.8	326	4	AAU13694	Aau13694 Arabidops	202	33	53.2	89	7	ADC27561	ADC27561 Human col
130	34	54.8	326	4	AAU13694	Aau13694 Arabidops	203	33	53.2	91	9	ABE36350	ABE36350 L. pneumo
131	34	54.8	326	4	AAU13694	Aau13694 Arabidops	204	33	53.2	99	4	ABG24120	ABG24120 Novel hum
132	34	54.8	326	4	AAU13694	Aau13694 Arabidops	205	33	53.2	105	9	ABE36350	ABE36350 L. pneumo
133	34	54.8	326	4	AAU13694	Aau13694 Arabidops	206	33	53.2	110	8	ADH80301	ADH80301 Plant ful
134	34	54.8	326	4	AAU13694	Aau13694 Arabidops	207	33	53.2	120	2	AAU59781	AAU59781 Human nor
135	34	54.8	326	4	AAU13694	Aau13694 Arabidops	208	33	53.2	120	2	AAU59781	AAU59781 Human nor
136	34	54.8	326	4	AAU13694	Aau13694 Arabidops	209	33	53.2	121	3	AAU59781	AAU59781 Human nor
137	34	54.8	326	4	AAU13694	Aau13694 Arabidops	210	33	53.2	121	3	AAU59781	AAU59781 Human nor
138	34	54.8	326	4	AAU13694	Aau13694 Arabidops	211	33	53.2	128	4	ABG24121	ABG24121 Novel hum
139	34	54.8	326	4	AAU13694	Aau13694 Arabidops	212	33	53.2	130	4	AAU59781	AAU59781 Human nor
140	34	54.8	326	4	AAU13694	Aau13694 Arabidops	213	33	53.2	130	4	AAU59781	AAU59781 Human nor
141	34	54.8	326	4	AAU13694	Aau13694 Arabidops	214	33	53.2	133	5	AAU59781	AAU59781 Human nor
142	34	54.8	326	4	AAU13694	Aau13694 Arabidops	215	33	53.2	142	7	ADL66005	ADL66005 C. glutam
143	34	54.8	326	4	AAU13694	Aau13694 Arabidops	216	33	53.2	142	7	ADL66005	ADL66005 C. glutam
144	34	54.8	326	4	AAU13694	Aau13694 Arabidops	217	33	53.2	164	10	AEF20612	Aef20612 Human ost
145	34	54.8	326	4	AAU13694	Aau13694 Arabidops	218	33	53.2	172	3	AAU59781	AAU59781 Human nor
146	34	54.8	326	4	AAU13694	Aau13694 Arabidops	219	33	53.2	172	3	AAU59781	AAU59781 Human nor
147	34	54.8	326	4	AAU13694	Aau13694 Arabidops	220	33	53.2	172	3	AAU59781	AAU59781 Human nor
148	34	54.8	326	4	AAU13694	Aau13694 Arabidops	221	33	53.2	172	3	AAU59781	AAU59781 Human nor
149	34	54.8	326	4	AAU13694	Aau13694 Arabidops	222	33	53.2	172	3	AAU59781	AAU59781 Human nor
150	34	54.8	326	4	AAU13694	Aau13694 Arabidops	223	33	53.2	172	3	AAU59781	AAU59781 Human nor
151	34	54.8	326	4	AAU13694	Aau13694 Arabidops	224	33	53.2	172	3	AAU59781	AAU59781 Human nor
152	34	54.8	326	4	AAU13694	Aau13694 Arabidops	225	33	53.2	172	3	AAU59781	AAU59781 Human nor
153	34	54.8	326	4	AAU13694	Aau13694 Arabidops	226	33	53.2	172	3	AAU59781	AAU59781 Human nor
154	34	54.8	326	4	AAU13694	Aau13694 Arabidops	227	33	53.2	172	3	AAU59781	AAU59781 Human nor
155	34	54.8	326	4	AAU13694	Aau13694 Arabidops	228	33	53.2	172	3	AAU59781	AAU59781 Human nor
156	34	54.8	326	4	AAU13694	Aau13694 Arabidops	229	33	53.2	172	3	AAU59781	AAU59781 Human nor
157	34	54.8	326	4	AAU13694	Aau13694 Arabidops	230	33	53.2	172	3	AAU59781	AAU59781 Human nor
158	34	54.8	326	4	AAU13694	Aau13694 Arabidops	231	33	53.2	172	3	AAU59781	AAU59781 Human nor
159	34	54.8	326	4	AAU13694	Aau13694 Arabidops	232	33	53.2	172	3	AAU59781	AAU59781 Human nor
160	34	54.8	326	4	AAU13694	Aau13694 Arabidops	233	33	53.2	172	3	AAU59781	AAU59781 Human nor
161	34	54.8	326	4	AAU13694	Aau13694 Arabidops	234	33	53.2	172	3	AAU59781	AAU59781 Human nor
162	34	54.8	326	4	AAU13694	Aau13694 Arabidops	235	33	53.2	172	3	AAU59781	AAU59781 Human nor
163	34	54.8	326	4	AAU13694	Aau13694 Arabidops	236	33	53.2	172	3	AAU59781	AAU59781 Human nor
164	34	54.8	326	4	AAU13694	Aau13694 Arabidops	237	33	53.2	172	3	AAU59781	AAU59781 Human nor
165	34	54.8	326	4	AAU13694	Aau13694 Arabidops	238	33	53.2	172	3	AAU59781	AAU59781 Human nor
166	34	54.8	326	4	AAU13694	Aau13694 Arabidops	239	33	53.2	172	3	AAU59781	AAU59781 Human nor
167	34	54.8	326	4	AAU13694	Aau13694 Arabidops	240	33	53.2	172	3	AAU59781	AAU59781 Human nor
168	34	54.8	326	4	AAU13694	Aau13694 Arabidops	241	33	53.2	172	3	AAU59781	AAU59781 Human nor
169	34	54.8	326	4	AAU13694	Aau13694 Arabidops	242	33	53.2	172	3	AAU59781	AAU59781 Human nor

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 9, 2006, 00:25:14 ; Search time 15.6 Seconds
(without alignments)
80.181 Million cell updates/sec

Title: US-10-797-626-1

Perfect score: 62

Sequence: 1 STQNALLSLTVC 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : PIR_80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	67.7	326	1 VGXRV	glycoprotein VP7 p
2	40	64.5	326	1 A48554	glycoprotein VP7 p
3	40	64.5	326	1 VGXRMI	glycoprotein VP7 p
4	40	64.5	326	1 VGXRMI	glycoprotein VP7 p
5	40	64.5	531	2 C97141	site-specific reco
6	39	62.9	812	1 PLMS	plasmin (EC 3.4.21
7	39	62.9	2493	2 S45734	probable membrane
8	37	59.7	601	2 T11677	probable transcrip
9	36	58.1	326	1 VGXRK4	glycoprotein VP7 p
10	36	58.1	560	2 S27874	steroid hormone re
11	36	58.1	812	1 PLBO	plasmin (EC 3.4.21
12	36	58.1	1313	2 T38943	probable guanine n
13	36	58.1	6805	2 S20901	titin - rabbit (fr
14	35.5	57.3	604	2 T15514	hypothetical prote
15	35	56.5	100	2 FN0619	hypothetical prote
16	35	56.5	115	2 S74763	hypothetical prote
17	35	56.5	211	2 A85098	hypothetical prote
18	35	56.5	211	2 C84775	probable harpin-in
19	35	56.5	326	1 VGXRAG	glycoprotein VP7 p
20	35	56.5	333	1 VHNZPM	nucleocapsid prote
21	35	56.5	456	2 G83449	probable MFS trans
22	35	56.5	718	2 F90512	hypothetical prote
23	34	54.8	62	2 C81101	hypothetical prote
24	34	54.8	120	2 A72617	hypothetical prote
25	34	54.8	179	2 AF0553	probable lipoprote
26	34	54.8	186	2 T16056	hypothetical prote
27	34	54.8	245	2 E87719	protein R119.3 [im
28	34	54.8	262	2 AB1196	enoyl- acyl-carrie
29	34	54.8	262	2 AH1553	enoyl- acyl-carrie

30	54.8	293	2	E83513	probable outer mem
31	54.8	308	2	T26007	hypothetical prote
32	54.8	391	2	S22579	translation initia
33	54.8	407	2	T06824	translation initia
34	54.8	468	1	B46114	glycoprotein gp13
35	54.8	468	1	VGBEER	glycoprotein gp13
36	54.8	492	2	AD2993	succinoglycan bios
37	54.8	493	2	F98290	exor protein limpo
38	54.8	551	2	F96624	hypothetical prote
39	54.8	551	2	B88949	protein R09B5.4 [i
40	54.8	573	2	C82525	hypothetical prote
41	54.8	1456	1	A36563	mannose receptor p
42	54.8	2048	1	ZLNZSE	genome polyprotein
43	54.8	2228	1	ZLNZSV	plasma (EC 3.4.21
44	53.2	120	2	E61545	orf6 protein - Aut
45	53.2	121	2	F44221	plasma (EC 3.4.21
46	53.2	123	2	C61545	hypothetical prote
47	53.2	131	2	A84448	hypothetical prote
48	53.2	197	2	AB2571	hypothetical prote
49	53.2	228	2	E86253	hypothetical prote
50	53.2	228	2	A31403	membrane protein B
51	53.2	244	2	A86873	transcription regu
52	53.2	257	2	C86784	pseudouridine synt
53	53.2	261	2	B86643	carbonyl reductase
54	53.2	279	2	T21099	hypothetical prote
55	53.2	312	2	T05529	magnesium-protopor
56	53.2	326	1	VGXRWL	glycoprotein VP7 p
57	53.2	326	2	JC4196	36K hydrophobic nu
58	53.2	327	2	JC4195	36K hydrophobic nu
59	53.2	399	2	D86460	F14W2.17 protein -
60	53.2	425	2	E88115	protein F53C3.11 [
61	53.2	428	1	EHHU	ig epsilon chain C
62	53.2	439	2	C94981	hypothetical prote
63	53.2	460	2	B61545	plasmin (EC 3.4.21
64	53.2	461	1	A46077	steroid hormone re
65	53.2	461	2	JC4972	steroidogenic fact
66	53.2	462	1	A56120	steroid hormone re
67	53.2	462	2	A40716	steroid hormone re
68	53.2	464	2	E89103	protein C18B10.4 [
69	53.2	464	2	A53101	vitamin D3 hydroxy
70	53.2	478	2	E90930	hypothetical prote
71	53.2	478	2	A85779	hypothetical prote
72	53.2	478	2	B64929	hypothetical prote
73	53.2	480	2	AF0704	conserved hypotet
74	53.2	501	1	A56543	Ftz-F1-related orp
75	53.2	519	2	D82536	conserved hypotet
76	53.2	535	2	D82536	hypothetical prote
77	53.2	623	2	T29139	hypothetical prote
78	53.2	644	2	T47835	hypothetical prote
79	53.2	714	2	E82507	hypothetical prote
80	53.2	740	2	T12223	NADH2 dehydrogenas
81	53.2	747	2	S66959	hypothetical prote
82	53.2	784	2	T43510	probable spindle p
83	53.2	810	1	PLHU	plasmin (EC 3.4.21
84	53.2	1012	2	B97326	endoglucanase fami
85	53.2	1042	2	T13647	hypothetical prote
86	53.2	1208	2	S69015	AXL1 protein - yea
87	53.2	1252	2	S36016	oocyst wall protei
88	53.2	1357	2	B96696	protein FIN21.4 [i
89	53.2	1433	2	S54587	mannose receptor p
90	53.2	1455	1	A48925	hypothetical prote
91	53.2	2102	2	T15626	hypothetical prote
92	53.2	2351	2	G71415	hypothetical prote
93	53.2	3295	2	AE0074	probable adhesin y
94	51.6	33	2	D61545	plasmin (EC 3.4.21
95	51.6	49	2	JH0641	rab protein Rab5c
96	51.6	160	2	F86283	protein T15D22.6 [
97	51.6	208	2	T21442	hypothetical prote
98	51.6	215	2	F34323	GTP-binding protei
99	51.6	215	2	A30413	GTP-binding protei
100	51.6	216	2	I38703	ras-related small
101	51.6	216	2	S65933	GTP-binding protei
102	51.6	251	2	T32318	hypothetical prote

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - protein search, using sw model
Run on: September 9, 2006, 00:11:36 ; Search time 129.74 Seconds
(without alignments)
92.687 Million cell updates/sec
Title: US-10-797-626-1
Perfect score: 62
Sequence: 1 STQNASLLSLTVC 13
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2849598 seqs, 925015592 residues
Total number of hits satisfying chosen parameters: 2849598
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries
Database : Uniprot 7.2.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	69.4	254	2	Q7THM5_9REOV
2	43	69.4	263	2	Q8QU19_9REOV
3	42	67.7	254	2	Q7THM3_9REOV
4	42	67.7	254	2	Q7THM4_9REOV
5	42	67.7	326	1	VS09_ROTTPB
6	42	67.7	326	2	Q86258_9REOV
7	42	67.7	326	2	Q86268_9REOV
8	42	67.7	326	2	Q86269_9REOV
9	42	67.7	326	2	Q9QC23_9REOV
10	42	67.7	702	2	Q9HM26_THEAC
11	40	64.5	84	2	Q6LSA1_PHOPR
12	40	64.5	263	2	Q8QU18_9REOV
13	40	64.5	263	2	Q8QU20_9REOV
14	40	64.5	263	2	Q8QU21_9REOV
15	40	64.5	263	2	Q8QU22_9REOV
16	40	64.5	263	2	Q8QU23_9REOV
17	40	64.5	263	2	Q8QU24_9REOV
18	40	64.5	263	2	Q8QU25_9REOV
19	40	64.5	263	2	Q8QU26_9REOV
20	40	64.5	263	2	Q8QU27_9REOV
21	40	64.5	263	2	Q8QU28_9REOV
22	40	64.5	263	2	Q8QU29_9REOV
23	40	64.5	263	2	Q8QU30_9REOV
24	40	64.5	263	2	Q8QU31_9REOV
25	40	64.5	263	2	Q8QU32_9REOV
26	40	64.5	263	2	Q8QU33_9REOV
27	40	64.5	263	2	Q8QU34_9REOV
28	40	64.5	263	2	Q8QU35_9REOV
29	40	64.5	263	2	Q8QU36_9REOV
30	40	64.5	263	2	Q8QU37_9REOV
31	40	64.5	326	1	VS09_ROTTPB

32	40	64.5	326	1	VS09_ROTTPB	P27423	porcine rot
33	40	64.5	326	1	VS09_ROTTPB	P32549	porcine rot
34	40	64.5	326	2	Q783Y5_9REOV	Q783Y5	human rotav
35	40	64.5	326	2	Q786Y4_9REOV	Q786Y4	human rotav
36	40	64.5	326	2	Q8B3A0_9REOV	Q8B3A0	human rotav
37	40	64.5	326	2	Q9PX10_9REOV	Q9PX10	human rotav
38	40	64.5	326	2	Q9PX38_9REOV	Q9PX38	human rotav
39	40	64.5	326	2	Q9QGR4_9REOV	Q9QGR4	human rotav
40	40	64.5	326	2	Q9QGR5_9REOV	Q9QGR5	human rotav
41	40	64.5	531	2	Q97HQ2_CLOAB	Q97HQ2	clostridium
42	40	64.5	1816	2	Q4RPB4_TETNG	Q4RPB4	tetradon n
43	39	62.9	254	2	Q7THM6_9REOV	Q7THM6	porcine rot
44	39	62.9	254	2	Q7THM7_9REOV	Q7THM7	porcine rot
45	39	62.9	326	2	Q6LSY6_9REOV	Q6LSY6	porcine rot
46	39	62.9	466	2	Q6TC10_MOUSE	Q6TC10	mus musculus
47	39	62.9	812	1	PLMN_MOUSE	PLMN	mouse
48	39	62.9	812	2	Q3V1T9_MOUSE	Q3V1T9	mouse
49	39	62.9	2493	1	YBA4_YEAST	YBA4	saccharomyc
50	38	61.3	84	2	Q8JYM8_9REOV	Q8JYM8	bovine rota
51	38	61.3	94	2	Q37389_CCPV1	Q37389	common chim
52	38	61.3	119	2	Q5APL2_CANAL	Q5APL2	candida alb
53	38	61.3	172	2	Q7PX25_ANOGA	Q7PX25	anopheles g
54	38	61.3	214	2	Q567N4_BRARE	Q567N4	brachydanio
55	38	61.3	229	2	Q6M9T8_PARUM	Q6M9T8	parachlamyd
56	38	61.3	284	2	Q2VSHI_9GAMA	Q2VSHI	ovine herpe
57	38	61.3	396	2	Q510M0_ENTHI	Q510M0	entamoeba h
58	38	61.3	593	2	Q71S51_9ECHI	Q71S51	ophiopholis
59	38	61.3	1575	2	Q8SSN3_DICDI	Q8SSN3	dictyosteli
60	37	59.7	180	2	Q95KT4_MACMU	Q95KT4	macaca mula
61	37	59.7	185	2	Q50RL7_ENTHI	Q50RL7	entamoeba h
62	37	59.7	203	2	Q4T1B6_TETNG	Q4T1B6	tetradon n
63	37	59.7	215	2	Q2XKP2_PSEPU	Q2XKP2	pseudomonas
64	37	59.7	215	2	Q88GY6_PSEPK	Q88GY6	pseudomonas
65	37	59.7	254	2	Q7THM2_9REOV	Q7THM2	porcine rot
66	37	59.7	292	1	NAR5_HUMAN	NAR5	homo sapien
67	37	59.7	292	2	Q86W02_HUMAN	Q86W02	homo sapien
68	37	59.7	326	2	Q56663_9REOV	Q56663	rotavirus g
69	37	59.7	326	2	Q86508_9REOV	Q86508	rotavirus
70	37	59.7	330	2	Q5JBB0_HYMNA	Q5JBB0	hymenocalli
71	37	59.7	401	2	Q5CZT0_BRARE	Q5CZT0	brachydanio
72	37	59.7	407	2	Q2MJJ9_MAIZE	Q2MJJ9	zea mays
73	37	59.7	409	2	Q4T9R3_TETNG	Q4T9R3	tetradon n
74	37	59.7	430	2	Q4UC32_THEAN	Q4UC32	theileria a
75	37	59.7	460	2	Q88EP6_PSEPK	Q88EP6	pseudomonas
76	37	59.7	572	2	Q2XER1_PSEPU	Q2XER1	pseudomonas
77	37	59.7	601	1	UCP3_SCHPO	UCP3	schizosacch
78	37	59.7	795	2	Q5B8S6_EMENI	Q5B8S6	aspergillus
79	37	59.7	1110	2	Q4IA83_GIBZE	Q4IA83	gibberella
80	37	59.7	2228	1	L_SENDA	L_SENDA	sendai viru
81	37	59.7	2228	1	L_SENDO	L_SENDO	sendai viru
82	37	59.7	2229	2	Q38G5_9PARA	Q38G5	sendai viru
83	37	59.7	6781	1	R1AB_PEDV7	R1AB_PEDV7	p replicase
84	36	58.1	84	2	Q8JYM3_9REOV	Q8JYM3	bovine rota
85	36	58.1	84	2	Q8JYM6_9REOV	Q8JYM6	bovine rota
86	36	58.1	84	2	Q8JYN7_9REOV	Q8JYN7	bovine rota
87	36	58.1	131	2	Q9PUJ7_ALLMI	Q9PUJ7	alligator m
88	36	58.1	147	2	Q8XP98_CLOPE	Q8XP98	clostridium
89	36	58.1	153	2	Q5X4H1_LEGPA	Q5X4H1	legionella
90	36	58.1	221	2	Q4CSL9_TRYCR	Q4CSL9	trypanosoma
91	36	58.1	224	2	Q8B3I3_9REOV	Q8B3I3	human rotav
92	36	58.1	280	2	Q68QF8_9REOV	Q68QF8	bovine rota
93	36	58.1	293	2	Q61S86_CAEBR	Q61S86	caenorhabdi
94	36	58.1	299	2	O5LEJ7_BACFN	O5LEJ7	bacteroides
95	36	58.1	299	2	Q91E85_9REOV	Q91E85	human rotav
96	36	58.1	318	2	Q6MSW8_MYCMS	Q6MSW8	mycoplasma
97	36	58.1	326	1	VS07_ROTBJ	VS07	bovine rota
98	36	58.1	326	2	Q45NQ0_9REOV	Q45NQ0	human rotav
99	36	58.1	326	2	Q65698_9REOV	Q65698	bovine rota
100	36	58.1	326	2	Q6WKW7_9REOV	Q6WKW7	buffalo rot
101	36	58.1	326	2	Q77LU9_9REOV	Q77LU9	canine rota
102	36	58.1	326	2	Q783Y8_9REOV	Q783Y8	human rotav
103	36	58.1	326	2	Q786Y6_9REOV	Q786Y6	human rotav
104	36	58.1	326	2	Q808C2_9REOV	Q808C2	human rotav

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OM protein - protein search, using sw model

Run on: September 9, 2006, 00:29:13 ; Search time 24.18 Seconds
(without alignments)
47.059 Million cell updates/sec

Title: US-10-797-626-1

Perfect score: 62

Sequence: 1 STQNASLLSLTVC 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

- 1: /EMC Celerra_SID83/prodata/2/iaa/5_COMB.pep.*
- 2: /EMC Celerra_SID83/prodata/2/iaa/6_COMB.pep.*
- 3: /EMC Celerra_SID83/prodata/2/iaa/7_COMB.pep.*
- 4: /EMC Celerra_SID83/prodata/2/iaa/H_COMB.pep.*
- 5: /EMC Celerra_SID83/prodata/2/iaa/PCTUS_COMB.pep.*
- 6: /EMC Celerra_SID83/prodata/2/iaa/RE_COMB.pep.*
- 7: /EMC Celerra_SID83/prodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	62.9	812	1	US-08-248-629A-1
2	39	62.9	812	1	US-08-451-932-1
3	39	62.9	812	1	US-08-452-260-1
4	39	62.9	812	1	US-08-326-785-1
5	39	62.9	812	1	US-08-612-788-1
6	39	62.9	812	1	US-08-605-598B-1
7	39	62.9	812	1	US-08-429-743-1
8	39	62.9	812	1	US-08-866-735-1
9	39	62.9	812	1	US-09-066-028-1
10	39	62.9	812	2	US-09-192-012-3
11	39	62.9	812	2	US-09-335-325-1
12	39	62.9	812	2	US-08-991-761A-12
13	39	62.9	812	2	US-09-335-614-1
14	39	62.9	812	5	PCT-US95-05107-1
15	36	58.1	60	2	US-09-270-767-34098
16	36	58.1	60	2	US-09-270-767-49315
17	36	58.1	560	1	US-09-132-619-10
18	36	58.1	560	2	US-09-282-803B-10
19	36	58.1	560	2	US-09-510-654-10
20	36	58.1	812	2	US-08-991-761A-7
21	35	56.5	28	2	US-09-471-276-1203
22	35	56.5	277	2	US-09-134-000C-4158
23	35	56.5	326	1	US-07-603-133B-28
24	35	56.5	358	2	US-09-252-991A-16785
25	34	54.8	88	2	US-09-270-767-34248
26	34	54.8	88	2	US-09-270-767-49465

27	34	54.8	183	2	US-09-902-540-12204	Sequence 12204, A
28	34	54.8	229	2	US-09-270-767-35290	Sequence 35290, A
29	34	54.8	229	2	US-09-270-767-50507	Sequence 50507, A
30	34	54.8	296	2	US-09-134-000C-4992	Sequence 4992, Ap
31	34	54.8	314	2	US-09-252-991A-19600	Sequence 19600, A
32	34	54.8	388	2	US-09-596-196-4	Sequence 4, Appli
33	34	54.8	439	2	US-09-248-796A-15969	Sequence 15969, A
34	34	54.8	442	2	US-09-248-796A-15434	Sequence 15434, A
35	34	54.8	508	2	US-09-248-796A-20809	Sequence 20809, A
36	34	54.8	582	2	US-09-248-796A-16870	Sequence 16870, A
37	34	54.8	1456	2	US-09-976-594-168	Sequence 168, App
38	33	53.2	29	2	US-09-203-258-281	Sequence 281, App
39	33	53.2	29	2	US-10-004-860-281	Sequence 281, App
40	33	53.2	71	2	US-09-205-258-355	Sequence 355, App
41	33	53.2	71	2	US-10-004-860-355	Sequence 355, App
42	33	53.2	77	2	US-09-483-846B-1	Sequence 1, Appli
43	33	53.2	103	2	US-09-248-796A-27448	Sequence 27448, A
44	33	53.2	115	2	US-09-949-016-9039	Sequence 9039, Ap
45	33	53.2	120	2	US-09-270-767-44612	Sequence 44612, A
46	33	53.2	186	2	US-10-104-047-2146	Sequence 2146, Ap
47	33	53.2	228	1	US-08-417-495-27	Sequence 27, Appl
48	33	53.2	228	1	US-08-284-391B-27	Sequence 27, Appl
49	33	53.2	228	2	US-09-218-950-27	Sequence 27, Appl
50	33	53.2	228	2	US-08-394-388A-27	Sequence 27, Appl
51	33	53.2	228	5	PCT-US92-01785-27	Sequence 27, Appl
52	33	53.2	228	5	PCT-US95-00454-27	Sequence 27, Appl
53	33	53.2	294	2	US-09-328-352-5549	Sequence 5549, Ap
54	33	53.2	294	2	US-09-328-352-6415	Sequence 6415, Ap
55	33	53.2	323	1	US-08-132-619-4	Sequence 4, Appli
56	33	53.2	323	2	US-09-282-803B-4	Sequence 4, Appli
57	33	53.2	323	2	US-09-510-654-4	Sequence 4, Appli
58	33	53.2	323	2	US-09-248-796A-16328	Sequence 16328, A
59	33	53.2	326	2	US-09-058-389A-3	Sequence 3, Appli
60	33	53.2	326	2	US-09-611-781-3	Sequence 3, Appli
61	33	53.2	346	2	US-08-808-701A-32	Sequence 32, Appl
62	33	53.2	359	2	US-09-270-767-59191	Sequence 59191, A
63	33	53.2	388	2	US-09-949-016-7631	Sequence 7631, Ap
64	33	53.2	451	2	US-09-377-250-4	Sequence 1, Appli
65	33	53.2	452	2	US-09-377-250-4	Sequence 4, Appli
66	33	53.2	453	2	US-09-489-039A-10288	Sequence 10288, A
67	33	53.2	456	2	US-09-058-389A-2	Sequence 2, Appli
68	33	53.2	456	2	US-09-611-781-2	Sequence 2, Appli
69	33	53.2	457	2	US-09-949-016-7211	Sequence 7211, Ap
70	33	53.2	466	2	US-09-949-016-9704	Sequence 9704, Ap
71	33	53.2	479	1	US-08-899-514-2	Sequence 2, Appli
72	33	53.2	495	1	US-08-132-619-2	Sequence 2, Appli
73	33	53.2	495	2	US-09-282-803B-2	Sequence 2, Appli
74	33	53.2	495	2	US-09-510-654-2	Sequence 2, Appli
75	33	53.2	495	2	US-09-949-016-6419	Sequence 6419, Ap
76	33	53.2	500	1	US-09-132-619-8	Sequence 8, Appli
77	33	53.2	500	2	US-09-282-803B-8	Sequence 8, Appli
78	33	53.2	500	2	US-09-510-654-8	Sequence 8, Appli
79	33	53.2	505	2	US-09-949-016-7067	Sequence 7067, Ap
80	33	53.2	541	1	US-09-132-619-6	Sequence 6, Appli
81	33	53.2	541	2	US-09-282-803B-6	Sequence 6, Appli
82	33	53.2	541	2	US-09-510-654-6	Sequence 6, Appli
83	33	53.2	568	3	US-09-946-893C-5	Sequence 5, Appli
84	33	53.2	570	3	US-09-946-893C-8	Sequence 8, Appli
85	33	53.2	575	3	US-09-946-893C-6	Sequence 6, Appli
86	33	53.2	625	2	US-09-583-545-2	Sequence 2, Appli
87	33	53.2	625	2	US-09-617-594A-6	Sequence 6, Appli
88	33	53.2	625	2	US-10-209-507-6	Sequence 6, Appli
89	33	53.2	695	2	US-09-270-767-43792	Sequence 43792, A
90	33	53.2	790	1	US-08-469-486-54	Sequence 54, Appl
91	33	53.2	790	3	US-08-469-658-54	Sequence 54, Appl
92	33	53.2	790	3	US-09-657-431A-1	Sequence 1, Appli
93	33	53.2	791	1	US-08-643-219-1	Sequence 1, Appli
94	33	53.2	791	1	US-09-131-995-1	Sequence 1, Appli
95	33	53.2	791	1	US-08-832-087B-1	Sequence 1, Appli
96	33	53.2	791	2	US-08-851-350-1	Sequence 1, Appli
97	33	53.2	791	2	US-09-132-154-1	Sequence 1, Appli
98	33	53.2	791	2	US-08-991-761A-6	Sequence 6, Appli
99	33	53.2	791	2	US-08-924-287A-1	Sequence 1, Appli

100	33	53.2	791	2	US-10-360-101-257	Sequence 257, Appl	173	31	50.0	270	2	US-09-252-991A-19031	Sequence 19031, A
101	33	53.2	810	1	US-07-854-603-2	Sequence 2, Appli	174	31	50.0	274	2	US-09-270-767-44349	Sequence 44349, A
102	33	53.2	810	1	US-08-147-000B-29	Sequence 29, Appl	175	31	50.0	295	2	US-09-495-406-18	Sequence 18, Appl
103	33	53.2	810	2	US-09-086-514-1	Sequence 1, Appli	176	31	50.0	295	2	US-09-816-028A-32	Sequence 32, Appl
104	33	53.2	810	2	US-09-192-012-5	Sequence 5, Appli	177	31	50.0	295	2	US-10-303-162-32	Sequence 32, Appl
105	33	53.2	810	2	US-09-403-736-1	Sequence 1, Appli	178	31	50.0	295	2	US-10-303-134-32	Sequence 32, Appl
106	33	53.2	810	2	US-09-701-265-1	Sequence 1, Appli	179	31	50.0	295	2	US-10-303-118-32	Sequence 32, Appl
107	33	53.2	810	3	US-09-946-893C-2	Sequence 2, Appli	180	31	50.0	295	2	US-10-303-128-32	Sequence 32, Appl
108	33	53.2	810	7	5200340-8	Patent No. 5200340	181	31	50.0	295	3	US-10-735-419-32	Sequence 32, Appl
109	33	53.2	814	1	US-08-750-711-1	Sequence 1, Appli	182	31	50.0	326	1	US-07-603-133B-22	Sequence 22, Appl
110	33	53.2	1113	2	US-09-949-016-9904	Sequence 9904, Ap	183	31	50.0	326	1	US-07-603-133B-23	Sequence 23, Appl
111	33	53.2	1433	2	US-09-487-558B-60	Sequence 60, Appl	184	31	50.0	326	2	US-08-089-397A-13	Sequence 13, Appl
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OM protein - protein search, using sw model

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Title: US-10-797-626-1

Perfect score: 62

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Scoring table: BLOSUM62

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Searched: 2097797 seqs, 463214858 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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119	34	54.8	525	4	US-10-424-599-215406	Sequence 215406,	192	33	53.2	164	6	US-11-166-412-225	Sequence 412, App
120	34	54.8	529	5	US-10-732-923-222301	Sequence 22301, A	193	33	53.2	172	5	US-10-467-657-4514	Sequence 4514, Ap
121	34	54.8	529	4	US-10-425-115-351332	Sequence 351332,	194	33	53.2	180	4	US-10-425-115-326102	Sequence 326102,
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123	34	54.8	531	4	US-10-424-599-229987	Sequence 229987,	196	33	53.2	186	6	US-11-072-512-2146	Sequence 2146, Ap
124	34	54.8	531	5	US-10-732-923-222307	Sequence 22307, A	197	33	53.2	197	4	US-10-424-599-152633	Sequence 152633,
125	34	54.8	531	5	US-10-732-923-222309	Sequence 22309, A	198	33	53.2	205	4	US-10-408-765A-2918	Sequence 2918, Ap
126	34	54.8	532	5	US-10-732-923-22232	Sequence 22252, A	199	33	53.2	213	4	US-10-023-386-3754	Sequence 3754, A
127	34	54.8	532	5	US-10-732-923-222310	Sequence 22310, A	200	33	53.2	216	4	US-10-023-386-3754	Sequence 3754, A
128	34	54.8	532	5	US-10-732-923-222312	Sequence 22312, A	201	33	53.2	228	3	US-09-939-537-27	Sequence 537, Ap
129	34	54.8	533	4	US-10-310-154-699	Sequence 699, App	202	33	53.2	228	3	US-09-243-008-27	Sequence 27, Appl
130	34	54.8	533	5	US-10-732-923-611	Sequence 611, App	203	33	53.2	228	4	US-10-079-130-4	Sequence 4, Appli
131	34	54.8	534	4	US-10-425-115-358372	Sequence 358372,	204	33	53.2	244	4	US-10-616-897-15	Sequence 15, Appl
132	34	54.8	539	4	US-10-425-114-54996	Sequence 54996, A	205	33	53.2	244	4	US-10-616-897-17	Sequence 17, Appl
133	34	54.8	539	4	US-10-425-114-56043	Sequence 56043, A	206	33	53.2	261	4	US-10-369-493-48303	Sequence 48303, A
134	34	54.8	539	5	US-10-732-923-222308	Sequence 22308, A	207	33	53.2	277	4	US-10-267-502-332	Sequence 332, App
135	34	54.8	540	4	US-10-424-599-276231	Sequence 276231,	208	33	53.2	277	6	US-11-097-143-24675	Sequence 24675, A
136	34	54.8	543	5	US-10-732-923-222300	Sequence 22300, A	209	33	53.2	283	4	US-10-616-897-4	Sequence 4, Appli
137	34	54.8	624	4	US-10-032-585-7797	Sequence 7797, Ap	210	33	53.2	286	4	US-10-616-897-4	Sequence 4, Appli
138	34	54.8	658	4	US-10-425-114-63115	Sequence 63115, A	211	33	53.2	288	4	US-10-616-897-2	Sequence 2, Appli
139	34	54.8	693	5	US-10-714-995-24	Sequence 24, Appl	212	33	53.2	297	6	US-11-097-143-31473	Sequence 31473, A
140	34	54.8	693	6	US-11-097-143-10674	Sequence 10674, A	213	33	53.2	310	6	US-11-166-412-224	Sequence 224, App
141	34	54.8	849	5	US-10-450-763-59554	Sequence 59554, A	214	33	53.2	326	3	US-09-284-320-88	Sequence 88, Appl
142	34	54.8	994	5	US-10-450-763-56037	Sequence 56037, A	215	33	53.2	346	3	US-09-808-701A-32	Sequence 32, Appl
143	34	54.8	1022	4	US-10-437-963-127708	Sequence 127708,	216	33	53.2	346	4	US-10-233-131-32	Sequence 32, Appl
144	34	54.8	1033	4	US-10-425-115-343179	Sequence 343179,	217	33	53.2	346	4	US-10-240-145-84	Sequence 84, Appl
145	34	54.8	1079	4	US-10-425-115-205898	Sequence 205898,	218	33	53.2	346	5	US-10-291-128-84	Sequence 84, Appl
146	34	54.8	1145	5	US-10-425-114-70456	Sequence 70456, A	219	33	53.2	354	6	US-11-188-298-15654	Sequence 15654, A
147	34	54.8	1184	5	US-10-450-763-51085	Sequence 51085, A	220	33	53.2	355	6	US-11-166-412-223	Sequence 223, App
148	34	54.8	1266	6	US-11-097-143-32124	Sequence 32124, A	221	33	53.2	374	3	US-11-188-298-13217	Sequence 13217, A
149	34	54.8	1456	3	US-09-870-759-95	Sequence 95, Appl	222	33	53.2	374	3	US-09-798-584-1	Sequence 1, Appli
150	34	54.8	1456	3	US-09-751-708A-95	Sequence 95, Appl	223	33	53.2	374	4	US-10-146-733-41	Sequence 41, Appl
151	34	54.8	1456	4	US-10-235-027-1217	Sequence 1217, Ap	224	33	53.2	374	4	US-10-257-022-6	Sequence 6, Appli
152	34	54.8	1456	4	US-10-428-817A-91	Sequence 91, Appl	225	33	53.2	374	4	US-10-074-978A-194	Sequence 194, App
153	34	54.8	1456	5	US-10-723-860-673	Sequence 673, App	226	33	53.2	378	4	US-10-437-963-194391	Sequence 194391,
154	34	54.8	1456	5	US-10-937-758A-72	Sequence 72, Appl	227	33	53.2	382	4	US-10-425-114-37688	Sequence 37688, A
155	33	53.2	29	3	US-09-933-767-281	Sequence 281, App	228	33	53.2	387	4	US-10-767-701-45657	Sequence 45657, A
156	33	53.2	29	4	US-10-004-860-281	Sequence 281, App	229	33	53.2	388	6	US-11-096-568A-21682	Sequence 21682, A
157	33	53.2	29	4	US-10-023-282-281	Sequence 281, App	230	33	53.2	394	4	US-10-437-963-177158	Sequence 177158,
158	33	53.2	44	4	US-09-864-761-36103	Sequence 36103, A	231	33	53.2	395	4	US-10-437-963-177156	Sequence 177156,
159	33	53.2	48	4	US-10-425-115-196785	Sequence 196785,	232	33	53.2	412	6	US-11-087-099-10691	Sequence 10691, A
160	33	53.2	55	4	US-10-437-963-133206	Sequence 133206,	233	33	53.2	416	4	US-10-282-122A-72263	Sequence 72263, A
161	33	53.2	68	4	US-10-424-599-152676	Sequence 152676,	234	33	53.2	421	4	US-10-282-122A-70083	Sequence 70083, A
162	33	53.2	71	3	US-09-933-767-355	Sequence 355, App	235	33	53.2	427	3	US-09-847-208-5	Sequence 5, Appli
163	33	53.2	71	4	US-10-004-860-355	Sequence 355, App	236	33	53.2	427	4	US-09-000-439-5	Sequence 5, Appli
164	33	53.2	71	4	US-10-023-282-355	Sequence 355, App	237	33	53.2	428	3	US-09-916-230-1	Sequence 1, Appli
165	33	53.2	74	6	US-11-188-298-7364	Sequence 7364, Ap	238	33	53.2	428	3	US-09-949-375A-1	Sequence 1, Appli
166	33	53.2	84	4	US-10-425-115-287801	Sequence 287801,	239	33	53.2	428	4	US-10-047-542-60	Sequence 60, Appl
167	33	53.2	86	4	US-10-424-599-268163	Sequence 268163,	240	33	53.2	428	5	US-10-363-954A-1	Sequence 1, Appli
168	33	53.2	86	4	US-10-767-701-56155	Sequence 56155, A	241	33	53.2	428	5	US-10-493-909-60	Sequence 60, Appl
169	33	53.2	99	5	US-10-450-763-54479	Sequence 54479, A	242	33	53.2	441	3	US-09-949-375A-7	Sequence 7, Appli
170	33	53.2	105	6	US-11-075-351-55	Sequence 55, Appl	243	33	53.2	441	3	US-10-363-954A-7	Sequence 7, Appli
171	33	53.2	107	4	US-10-425-115-223798	Sequence 223798,	244	33	53.2	446	5	US-10-732-923-22261	Sequence 22261, A
172	33	53.2	110	4	US-10-425-114-49667	Sequence 49667, A	245	33	53.2	456	5	US-10-756-149-5775	Sequence 5775, Ap
173	33	53.2	125	4	US-10-425-115-349493	Sequence 349493,	246	33	53.2	457	4	US-10-424-599-208072	Sequence 208072,

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OM protein - protein search, using sw model

Run on: September 9, 2006, 00:11:07 ; Search time 140.98 Seconds
(without alignments)
61.619 Million cell updates/sec

Title: US-10-797-626-2

Perfect score: 94
Sequence: 1 KGCSTONQALLSLIVGKA 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 segs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : A_Geneseq_8:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*
- 9: Geneseqp2005s:*
- 10: Geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	94	100.0	19	ADS18078	Ads18078 Laminin s
2	74.5	79.3	18	ADS18079	Ads18079 Laminin s
3	45	47.9	324	ABO80324	ABO80324 Pseudomon
4	45	47.9	371	ABO81209	ABO81209 Pseudomon
5	44	46.8	865	AAG78665	Aag78665 Moritella
6	43	45.7	13	ADS18077	Ads18077 Laminin s
7	43	45.7	139	AAU33241	AAU33241 Novel hum
8	43	45.7	235	ABU34024	ABU34024 Protein e
9	43	45.7	337	ABU00184	ABU00184 Human nov
10	43	45.7	449	ABU71938	ABU71938 Drosophil
11	43	45.7	449	AAU74634	AAU74634 Oestrogen
12	43	45.7	452	ABU10110	ABU10110 Mouse cas
13	43	45.7	452	ADB79812	ADB79812 Rat caspa
14	43	45.7	452	ADE63000	ADE63000 Rat Prote
15	43	45.7	621	ADQ67726	ADQ67726 Novel hum
16	43	45.7	751	ABG69453	ABG69453 Human nov
17	43	45.7	751	ABU60658	ABU60658 Human kin
18	43	45.7	751	ADH62285	ADH62285 Novel hum
19	43	45.7	751	10 AEE28231	Aee28231 Human kin
20	43	45.7	764	5 ABG69452	ABG69452 Human nov
21	43	45.7	764	5 ABU60657	ABU60657 Human kin
22	43	45.7	764	8 ADH62283	ADH62283 Novel hum
23	43	45.7	764	10 AEE28229	Aee28229 Human kin

24	43	45.7	776	5 ABG69461	ABG69461 Human nov
25	43	45.7	776	6 ABU60666	ABU60666 Human kin
26	43	45.7	776	8 ADH62301	ADH62301 Novel hum
27	43	45.7	776	10 AEE28247	Aee28247 Human kin
28	43	45.7	789	5 ABG69460	ABG69460 Human nov
29	43	45.7	789	6 ABU60665	ABU60665 Human kin
30	43	45.7	789	8 ADH62299	ADH62299 Novel hum
31	43	45.7	789	10 AEE28245	Aee28245 Human kin
32	43	45.7	838	5 ABG69469	ABG69469 Human nov
33	43	45.7	838	6 ABU60674	ABU60674 Human kin
34	43	45.7	838	8 ADH62317	ADH62317 Novel hum
35	43	45.7	838	10 AEE28263	Aee28263 Human kin
36	43	45.7	851	5 ABG69468	ABG69468 Human nov
37	43	45.7	851	6 ABU60673	ABU60673 Human kin
38	43	45.7	851	8 ADH62315	ADH62315 Novel hum
39	43	45.7	851	10 AEE28261	Aee28261 Human kin
40	43	45.7	863	5 ABG69465	ABG69465 Human nov
41	43	45.7	863	6 ABU60670	ABU60670 Human kin
42	43	45.7	863	8 ADH62309	ADH62309 Novel hum
43	43	45.7	863	10 AEE28255	Aee28255 Human kin
44	43	45.7	864	5 ABG69451	ABG69451 Human nov
45	43	45.7	864	6 ABU60656	ABU60656 Human kin
46	43	45.7	864	8 ADH62281	ADH62281 Novel hum
47	43	45.7	864	10 AEE28227	Aee28227 Human kin
48	43	45.7	870	5 ABG69450	ABG69450 Human nov
49	43	45.7	870	6 ABU60655	ABU60655 Human kin
50	43	45.7	870	8 ADH62279	ADH62279 Novel hum
51	43	45.7	870	10 AEE28225	Aee28225 Human kin
52	43	45.7	876	5 ABG69464	ABG69464 Human nov
53	43	45.7	876	6 ABU60669	ABU60669 Human kin
54	43	45.7	876	8 ADH62307	ADH62307 Novel hum
55	43	45.7	876	10 AEE28253	Aee28253 Human kin
56	43	45.7	889	5 ABG69459	ABG69459 Human nov
57	43	45.7	889	6 ABU60664	ABU60664 Human kin
58	43	45.7	889	8 ADH62297	ADH62297 Novel hum
59	43	45.7	889	10 AEE28243	Aee28243 Human kin
60	43	45.7	895	5 ABG69458	ABG69458 Human nov
61	43	45.7	895	6 ABU60663	ABU60663 Human kin
62	43	45.7	895	8 ADH62295	ADH62295 Novel hum
63	43	45.7	895	10 AEE28241	Aee28241 Human kin
64	43	45.7	951	5 ABG69467	ABG69467 Human nov
65	43	45.7	951	6 ABU60672	ABU60672 Human kin
66	43	45.7	951	8 ADH62313	ADH62313 Novel hum
67	43	45.7	951	10 AEE28259	Aee28259 Human kin
68	43	45.7	957	5 ABG69466	ABG69466 Human nov
69	43	45.7	957	6 ABU60671	ABU60671 Human kin
70	43	45.7	957	8 ADH62311	ADH62311 Novel hum
71	43	45.7	957	10 AEE28257	Aee28257 Human kin
72	43	45.7	976	5 ABG69463	ABG69463 Human nov
73	43	45.7	976	6 ABU60668	ABU60668 Human kin
74	43	45.7	976	8 ADH62305	ADH62305 Novel hum
75	43	45.7	976	10 AEE28251	Aee28251 Human kin
76	43	45.7	982	5 ABG69462	ABG69462 Human nov
77	43	45.7	982	6 ABU60667	ABU60667 Human kin
78	43	45.7	982	8 ADH62303	ADH62303 Novel hum
79	43	45.7	982	10 AEE28249	Aee28249 Human kin
80	43	45.7	1270	7 ADJ70447	ADJ70447 Human hea
81	43	45.7	1270	9 AEA52444	AEA52444 Human tau
82	43	45.7	1308	6 ABR57072	ABR57072 Human tau
83	43	45.7	1308	9 ADV97846	ADV97846 Murine pr
84	43	45.7	1321	8 ADN07671	ADN07671 Human bra
85	43	45.7	1331	7 ADC10010	ADC10010 Human NOV
86	42	44.7	313	4 ABG09606	ABG09606 Novel hum
87	42	44.7	330	4 ABG02784	ABG02784 Novel hum
88	42	44.7	719	2 AAR25069	Aar25069 mLiF-R. 3
89	42	44.7	719	2 AAR45775	Aar45775 Murine le
90	42	44.7	719	2 AAR49507	Aar49507 Human LiF
91	42	44.7	719	2 AAR74096	Aar74096 Murine le
92	42	44.7	1092	8 ABO84694	ABO84694 Mouse can
93	41	43.6	122	7 ADF59526	ADF59526 Human pol
94	41	43.6	154	4 ABG23905	ABG23905 Novel hum
95	41	43.6	167	7 ADM25939	ADM25939 Hyperther
96	41	43.6	263	8 ADT89334	ADT89334 Mouse onc

97	41	43.6	263	9	AED01095	Aed01095 Mouse onc	170	39	41.5	376	3	AA55841	Aay55841 Human cyt
98	41	43.6	421	4	ABB63148	Abb63148 Drosophila	171	39	41.5	376	7	ADD14094	Add14094 Human src
99	41	43.6	428	4	ABB60476	Abb60476 Drosophila	172	39	41.5	376	7	AD59314	Ad59314 Human pro
100	41	43.6	431	4	ABG15132	Abg15132 Novel hum	173	39	41.5	376	7	ADF76331	Adf76331 Novel hum
101	41	43.6	476	7	ADF28933	Adf28933 Sheep ang	174	39	41.5	376	8	ADI53096	Adi53096 Human gra
102	41	43.6	1154	6	ADAI3344	Adai3344 Human int	175	39	41.5	376	8	ADL83201	Adl83201 Human pro
103	41	43.6	1401	8	ADLI3306	Adli3306 Human ste	176	39	41.5	376	8	ADP24324	Adp24324 PRO poly
104	41	43.6	1401	9	ADL07508	Adl07508 Cyclin-de	177	39	41.5	376	8	ADT98544	Adt98544 Human ser
105	41	43.6	1634	2	AAR42452	Aar42452 Enzyme in	178	39	41.5	376	8	ABP29701	Abp29701 Streptoco
106	41	43.6	1642	2	AAR89400	Aar89400 S. putref	179	39	41.5	398	5	ABP30071	Abp30071 Streptoco
107	41	43.6	2756	2	AAR99462	Aar99462 Biosynthe	180	39	41.5	398	8	ADV88303	Adv88303 Streptoco
108	41	43.6	2756	3	AAB37050	Aab37050 S. putref	181	39	41.5	398	8	ADV9556	Adv9556 Streptoco
109	41	43.6	2756	3	AAB10467	Aab10467 Shewanell	182	39	41.5	398	8	ADV81725	Adv81725 Streptoco
110	41	43.6	2756	4	AAG64455	Aag64455 S. putref	183	39	41.5	398	6	ABU39183	Abu39183 Protein e
111	40.5	43.1	254	6	ABU33391	Abu33391 Protein e	184	39	41.5	400	6	ADT49283	Adt49283 Pectate 1
112	40.5	43.1	254	9	ABE39665	Aeb39665 L. pneumo	185	39	41.5	466	8	ABO71642	Ab071642 Pseudomon
113	40.5	43.1	261	9	ABE36245	Aeb36245 L. pneumo	186	39	41.5	485	7	AED26464	Aed26464 Novel hum
114	40.5	43.1	332	4	AAB76570	Aab76570 Corynebac	187	39	41.5	529	9	ADG27693	Adg27693 Human nov
115	40.5	43.1	332	4	AAG92306	Aag92306 C. glutami	188	39	41.5	530	4	AAU30834	Aau30834 Novel hum
116	40.5	43.1	587	4	AAB49986	Aab49986 P. gallin	189	39	41.5	566	4	AAU30834	Aau30834 Novel hum
117	40	42.6	115	4	AAU45567	Aau45567 Propionib	190	39	41.5	582	4	ABB63987	Abb63987 Drosophila
118	40	42.6	115	6	ABM42086	Abm42086 Propionib	191	39	41.5	826	3	ABY95050	AbY95050 Candida a
119	40	42.6	142	3	AAG57167	Aag57167 Arabidops	192	39	41.5	1049	8	ADN18867	Adn18867 Bacterial
120	40	42.6	192	4	AAU46473	Aau46473 Propionib	193	39	41.5	1184	4	ABG20726	Abg20726 Novel hum
121	40	42.6	192	6	ABM42992	Abm42992 Propionib	194	39	41.5	1450	6	ADA89491	Ada89491 Staphyloc
122	40	42.6	209	5	ABP26506	Abp26506 Streptoco	195	39	41.5	1456	6	AAU24033	Aar24033 Soluble m
123	40	42.6	248	8	ADL05903	Adl05903 M. catarr	196	39	41.5	1456	6	ABU79121	Abu79121 Anglostet
124	40	42.6	255	8	ADL95159	Adl95159 Plant ful	197	39	41.5	1456	7	ADF43375	Adf43375 Mannose r
125	40	42.6	278	6	ABU25195	Abu25195 Protein e	198	39	41.5	1456	7	ADN39899	Adn39899 Cancer/an
126	40	42.6	292	8	ADX67591	Adx67591 Plant ful	199	39	41.5	1456	7	ADN95147	Adn95147 Human BEC
127	40	42.6	431	4	AAB79671	Aab79671 Corynebac	200	39	41.5	1456	8	ADL12439	Adl12439 Human ste
128	40	42.6	436	8	ADM98815	Adm98815 HMG-CoA r	201	39	41.5	1456	8	ADQ17856	Adq17856 Human sof
129	40	42.6	436	8	ADS42948	Ads42948 Bacterial	202	39	41.5	1456	8	ADP23714	Adp23714 PRO poly
130	40	42.6	477	8	ADX87538	Adx87538 Plant ful	203	39	41.5	1456	9	AEA03046	Aea03046 Glycophor
131	40	42.6	563	7	ABO70641	Ab070641 Pseudomon	204	39	41.5	1491	6	AAU34072	Aau34072 Staphyloc
132	40	42.6	617	8	ADN24090	Adn24090 Bacterial	205	39	41.5	1499	6	ABU16457	Abu16457 Protein e
133	40	42.6	645	4	AAG82945	Aag82945 S. epider	206	39	41.5	1502	6	AAU36569	Aau36569 Staphyloc
134	40	42.6	933	6	ABU43104	Abu43104 Protein e	207	39	41.5	1502	6	ABM71608	Abm71608 Bacterial
135	40	42.6	1501	4	AAG82878	Aag82878 S. epider	208	39	41.5	1502	6	ADN19908	Adn19908 Bacterial
136	40	42.6	1509	6	ABU43942	Abu43942 Protein e	209	39	41.5	2335	8	ADN19908	Adn19908 Bacterial
137	40	42.6	1510	2	AAU01312	Aay01312 Glutamine	210	38.5	41.0	18	8	ADR42896	Adr42896 Denatured
138	40	42.6	1510	4	AAB79669	Aab79669 Corynebac	211	38.5	41.0	350	8	AAU87117	Aau87117 Novel cen
139	40	42.6	1510	4	AAG89953	Aag89953 C. glutami	212	38.5	41.0	350	8	ADI54432	Adi54432 Novel hum
140	40	42.6	1510	7	ADD13595	Adi13595 C. glutami	213	38.5	41.0	783	3	ABM23648	Abm23648 Murine pa
141	40	42.6	1529	5	ABP39100	Abp39100 Staphyloc	214	38.5	41.0	1006	2	AAW77290	Aaw77290 Human dif
142	40	42.6	1529	8	ADS07312	Ads07312 Staphyloc	215	38.5	41.0	1006	3	ABM23647	Abm23647 Human pap
143	39.5	42.0	203	4	ABM96735	Abm96735 Putative	216	38	40.4	18	8	ADH16067	Adh16067 Gliadin r
144	39.5	42.0	333	6	ABU39107	Abu39107 Protein e	217	38	40.4	18	8	ADH15337	Adh15337 Gliadin r
145	39.5	42.0	652	7	ABM88164	Abm88164 Rice abio	218	38	40.4	70	3	AAU40912	Aau40912 Human ORF
146	39.5	42.0	843	9	ABE13424	Aeb13424 Human pro	219	38	40.4	70	3	ABP08060	Abp08060 Human ORF
147	39.5	42.0	885	9	ABE13426	Aeb13426 Human pro	220	38	40.4	79	5	ADM69713	Adm69713 D melanog
148	39.5	42.0	898	4	ABG15488	Abg15488 Novel hum	221	38	40.4	91	10	ABE60259	Aee60259 Cat chlam
149	39.5	42.0	933	8	ADT77664	Adt77664 Splice va	222	38	40.4	192	2	AAU32780	Aay32780 HIV chemo
150	39.5	42.0	1604	4	AAU47327	Aau47327 FCPR4. 8/	223	38	40.4	192	5	ABP00179	Abp00179 Human ORF
151	39.5	42.0	2015	4	ABE65890	Abb65890 Drosophila	224	38	40.4	224	3	AAU20878	Aag20878 Arabidops
152	39	41.5	2015	4	ABE65890	Abb65890 Drosophila	225	38	40.4	224	3	AAU20878	Aag20878 Arabidops
153	39	41.5	87	4	AAU47327	Aau47327 FCPR4. 8/	226	38	40.4	224	7	ABO68854	Ab068854 Pseudomon
154	39	41.5	87	4	AAU47327	Aau47327 FCPR4. 8/	227	38	40.4	224	7	ABO68854	Ab068854 Pseudomon
155	39	41.5	156	8	ADO07062	Ado07062 Human tes	228	38	40.4	263	3	AAU50880	Aag50880 Arabidops
156	39	41.5	227	6	ABU38639	Abu38639 Protein e	229	38	40.4	263	3	AAU50880	Aag50880 Arabidops
157	39	41.5	238	5	ABP26194	Abp26194 Streptoco	230	38	40.4	324	7	ADL98001	Adl98001 Human olf
158	39	41.5	250	9	AED01099	Aed01099 Rat oncos	231	38	40.4	329	6	ABU43856	Abu43856 Protein e
159	39	41.5	269	6	ABU19123	Abu19123 Protein e	232	38	40.4	333	6	ABM67449	Abm67449 Photorehab
160	39	41.5	273	8	ADP24567	Adp24567 PRO poly	233	38	40.4	337	4	AAU79806	Aau79806 Human pro
161	39	41.5	297	7	ADH86302	Adh86302 Enterococ	234	38	40.4	337	4	AAU79806	Aau79806 Human pro
162	39	41.5	309	7	ABM85441	Abm85441 Human pro	235	38	40.4	357	6	ABU49081	Abu49081 Protein e
163	39	41.5	322	8	ADO07060	Ado07060 Human pro	236	38	40.4	369	5	ABP74089	Abp74089 Candida a
164	39	41.5	328	8	ABM82806	Abm82806 Human dia	237	38	40.4	381	4	AAU17874	Aau17874 C. glutami
165	39	41.5	328	8	ABM82805	Abm82805 Human dia	238	38	40.4	441	5	AAO17874	Aao17874 C. glutami
166	39	41.5	328	8	ABM82567	Abm82567 Human dia	239	38	40.4	441	9	AEC56408	Aec56408 Corynebacc
167	39	41.5	328	8	ABM82568	Abm82568 Human dia	240	38	40.4	468	6	ABP79583	Abp79583 N. gonorr
168	39	41.5	361	4	ABM60382	Abm60382 Drosophila	241	38	40.4	505	7	ADJ71088	Adj71088 Human hea
169	39	41.5	376	2	AAR99254	Aar99254 Cytoplasm	242	38	40.4	585	4	AAU36330	Aau36330 Pseudomon

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OM protein - protein search, using sw model

Run on: September 9, 2006, 00:25:14 ; Search time 22.8 Seconds
(without alignments)
80.181 Million cell updates/sec

Title: US-10-797-626-2

Perfect score: 94

Sequence: 1 KGGCSTQNAQLLSLVGKA 19

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

PIR_80.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	46.8	285	2	F84986 methenyltetrahydro
2	44	46.8	828	2	T23267 hypothetical prote
3	43	45.7	452	2	JG6507 caspase-2 - rat
4	42	44.7	71	2	T09239 nifu protein - Fra
5	42	44.7	1092	2	JX0312 differentiation-st
6	41	43.6	240	2	S53403 probable membrane
7	41	43.6	263	2	S64719 oncostatin M - mou
8	41	43.6	428	2	A43741 terminus protein -
9	41	43.6	476	1	JC2318 angiotensin precu
10	41	43.6	600	2	A25570 hypothetical prote
11	41	43.6	643	2	AC2199 phosphoenolpyruvat
12	41	43.6	1401	2	T02255 probable ubiquitou
13	41	43.6	2756	2	T30183 hypothetical prote
14	41	43.6	3295	2	A20074 probable adhesin Y
15	40	42.6	425	2	C72744 hypothetical prote
16	40	42.6	436	2	G59466 3-hydroxy-3-methyl
17	40	42.6	556	2	E95289 conserved hypotet
18	40	42.6	617	2	T15408 hypothetical prote
19	40	42.6	624	2	T29286 hypothetical prote
20	40	42.6	772	2	T16474 hypothetical prote
21	40	42.6	1751	2	T09394 gag-pro-poi polyp
22	39.5	42.0	203	2	E75145 lsu ribosomal prot
23	39.5	42.0	206	2	A71185 probable ribosomal
24	39.5	42.0	1811	2	T00035 nonstructural poly
25	39	41.5	139	2	D82296 transcription regu
26	39	41.5	227	2	D83162 respiratory nitrat
27	39	41.5	269	2	B70124 conserved hypotet
28	39	41.5	361	2	T13745 hypothetical prote
29	39	41.5	376	2	B59273 proteinase inhibit

30	39	41.5	437	2	AF0667	probable phosphotr
31	39	41.5	449	2	S76839	hypothetical prote
32	39	41.5	468	2	T08139	shaggy-like protei
33	39	41.5	476	2	AH2968	mannose-1-phosphat
34	39	41.5	476	2	C98314	mannose-1-phosphat
35	39	41.5	653	2	A84675	hypothetical prote
36	39	41.5	1049	1	S19421	ATP-dependent perm
37	39	41.5	1456	1	A36563	mannose receptor p
38	39	41.5	1499	2	A89813	glutamate synthase
39	39	41.5	1902	1	B44858	lactocepin (EC 3.4
40	39	41.5	2335	2	T40186	probable phosphati
41	38.5	41.0	820	2	T22172	hypothetical prote
42	38.5	41.0	1006	2	T00050	hypothetical prote
43	38	40.4	129	2	B83173	hypothetical prote
44	38	40.4	187	2	S32968	probable membrane
45	38	40.4	188	2	T52029	drmp kinase (EC 2.
46	38	40.4	195	2	H95297	probable allantoin
47	38	40.4	197	2	AB2571	hypothetical prote
48	38	40.4	244	2	F90801	HecB-like protein
49	38	40.4	273	2	T31892	hypothetical prote
50	38	40.4	348	2	G85661	hypothetical prote
51	38	40.4	357	2	D82337	UDP-N-acetylenolp
52	38	40.4	477	1	A29978	angiotensin precu
53	38	40.4	503	1	VMUT1B	variant surface gl
54	38	40.4	541	2	T43862	FAD flavoprotein o
55	38	40.4	546	2	AE0571	probable membrane
56	38	40.4	585	2	H83199	phosphotransferase
57	38	40.4	850	2	AE1954	hypothetical prote
58	38	40.4	907	2	T27317	hypothetical prote
59	38	40.4	928	2	T24868	hypothetical prote
60	38	40.4	1455	1	A48925	mannose receptor p
61	38	40.4	1902	2	S06997	lactocepin (EC 3.4
62	38	40.4	1902	2	B45764	lactocepin (EC 3.4
63	38	40.4	1962	2	A32634	lactocepin (EC 3.4
64	37.5	39.9	93	2	G70815	hypothetical prote
65	37	39.4	93	2	A84991	CT001 hypothetical
66	37	39.4	93	2	F72130	conserved hypotet
67	37	39.4	160	2	T25185	hypothetical prote
68	37	39.4	228	1	S18588	hypothetical mercu
69	37	39.4	237	2	B84377	hypothetical prote
70	37	39.4	267	2	S72583	abcl protein - Myc
71	37	39.4	288	1	JS0662	methylenetetrahydr
72	37	39.4	288	2	B85553	5,10-methylene-tet
73	37	39.4	288	2	AB0344	methenyltetrahydro
74	37	39.4	288	2	G90702	5,10-methylene-tet
75	37	39.4	295	2	S56302	hypothetical prote
76	37	39.4	341	2	S69802	N-acetylmuramoyl-L
77	37	39.4	340	2	D84050	L-cysteine sulfurt
78	37	39.4	425	2	D88115	protein F53C3.11 [
79	37	39.4	457	2	S03961	Ig mu chain C regi
80	37	39.4	473	2	A86989	conserved hypotet
81	37	39.4	477	1	ANET	angiotensin precu
82	37	39.4	506	2	H82991	exopolysphatase
83	37	39.4	578	2	B37852	phosphotransferase
84	37	39.4	581	2	B81909	exodeoxyribonuclea
85	37	39.4	702	2	T16832	hypothetical prote
86	37	39.4	935	2	S62476	hypothetical prote
87	37	39.4	946	2	A84133	hypothetical prote
88	37	39.4	1095	2	T31423	polyprotein allierg
89	37	39.4	1097	2	S17308	leukemia inhibitor
90	37	39.4	1347	2	T02214	ubiquitous TPR mot
91	37	39.4	2823	2	F87908	protein T22A3.8 [i
92	37	39.4	2823	2	T23064	hypothetical prote
93	37	39.4	3102	2	T43291	laminin alpha chai
94	36.5	38.8	249	2	F96511	hypothetical prote
95	36.5	38.8	262	2	T17442	ybt protein - yer
96	36.5	38.8	267	2	AH0232	yersiniabactin bio
97	36.5	38.8	267	2	T30344	irp4 protein - yer
98	36.5	38.8	267	2	T47050	hypothetical prote
99	36.5	38.8	342	2	AF3357	anthranilate phosph
100	36	38.3	55	2	B97548	hypothetical prote
101	36	38.3	76	2	AF2168	hypothetical prote
102	36	38.3	79	1	A58656	adipokinetic hormo

103	36	38.3	125	2	T27611	hypothetical prote	176	35	37.2	292	2	B95232	conserved hypothet
104	36	38.3	150	2	AH0371	probable membrane	177	35	37.2	293	2	F83618	conserved hypothet
105	36	38.3	178	2	G59856	hypothetical prote	178	35	37.2	294	2	T23682	hypothetical prote
106	36	38.3	227	2	E83288	probable ATP-bind	179	35	37.2	307	2	H71098	hypothetical prote
107	36	38.3	238	2	S77699	inner cell wall ma	180	35	37.2	309	2	AE0946	FdhE protein limpo
108	36	38.3	260	2	D75404	phosphatidylglycer	181	35	37.2	317	2	G72342	L-isocapartate(D-a
109	36	38.3	261	2	I52518	sperm acrosome ant	182	35	37.2	323	2	C89045	protein B0238.6 [i
110	36	38.3	263	2	AE0140	molybdenum transpo	183	35	37.2	325	2	C71040	hypothetical prote
111	36	38.3	293	2	H70366	lysyl-tRNA synthet	184	35	37.2	333	2	F83107	hypothetical prote
112	36	38.3	315	2	D48560	immediate-early pr	185	35	37.2	333	2	G71979	probable type II D
113	36	38.3	321	2	JC5460	intracellular alka	186	35	37.2	344	1	KHPGD	cathepsin D (EC 3.
114	36	38.3	322	2	G83922	intracellular alka	187	35	37.2	381	2	T13701	NADH2 dehydrogenas
115	36	38.3	323	2	AB1659	hypothetical prote	188	35	37.2	385	2	A84646	probable serpin [i
116	36	38.3	329	2	T27337	hypothetical prote	189	35	37.2	391	2	B64606	acetyl coenzyme A
117	36	38.3	350	2	AC0037	probable tellurite	190	35	37.2	391	2	T32706	hypothetical prote
118	36	38.3	351	2	D82891	conserved hypothet	191	35	37.2	397	2	A96925	uncharacterized co
119	36	38.3	376	2	B71652	iron-sulfur cofact	192	35	37.2	423	2	B70931	probable PFB prote
120	36	38.3	384	2	AH0662	probable chemo-rec	193	35	37.2	430	2	T33155	hypothetical prote
121	36	38.3	384	2	D90547	oligopeptide ABC t	194	35	37.2	430	2	S77393	cell division synth
122	36	38.3	400	2	S76446	hypothetical prote	195	35	37.2	430	2	I39727	mammopine biosynth
123	36	38.3	425	2	T12473	hypothetical prote	196	35	37.2	431	2	T16191	hypothetical prote
124	36	38.3	447	2	C70951	hypothetical prote	197	35	37.2	442	2	T42048	mom-1 protein - Ca
125	36	38.3	469	2	A41660	nitrogenase vanadi	198	35	37.2	445	2	T38916	probable transcript
126	36	38.3	489	2	T04596	hypothetical prote	199	35	37.2	451	2	JE0313	exoglucanase (EC 3
127	36	38.3	504	2	S09797	hypothetical prote	200	35	37.2	451	2	T62377	6-phosphogluconate
128	36	38.3	517	2	T04597	hypothetical prote	201	35	37.2	469	2	A72377	hypothetical prote
129	36	38.3	527	2	T38045	hypothetical prote	202	35	37.2	470	2	A87298	hypothetical prote
130	36	38.3	531	2	C97141	probable t-complex	203	35	37.2	482	2	T16834	hypothetical prote
131	36	38.3	533	2	A86433	site-specific reco	204	35	37.2	486	2	C86645	Glu-tRNA amidotran
132	36	38.3	561	2	A11409	potassium-transpor	205	35	37.2	491	2	B96633	hypothetical prote
133	36	38.3	561	2	AH1785	potassium-transpor	206	35	37.2	510	2	F90710	citrate lyase alph
134	36	38.3	567	2	E84658	hypothetical prote	207	35	37.2	510	2	B64795	citrate (pro-3s)-l
135	36	38.3	614	2	A82832	protein-export mem	208	35	37.2	510	2	B85561	citrate lyase alph
136	36	38.3	747	2	A29299	two component resp	209	35	37.2	535	2	T23419	hypothetical prote
137	36	38.3	758	2	T02925	protoporphyrin IX	210	35	37.2	537	2	T27612	hypothetical prote
138	36	38.3	775	1	EDBE11	immediate-early pr	211	35	37.2	558	2	B48492	polysaccharide exp
139	36	38.3	783	2	A98353	probable transcript	212	35	37.2	558	2	T04598	hypothetical prote
140	36	38.3	821	2	S67087	hypothetical prote	213	35	37.2	565	2	S10367	hypothetical prote
141	36	38.3	835	1	S67669	transitional endop	214	35	37.2	589	2	A82504	carboxylesterase (
142	36	38.3	841	2	T14398	S-receptor kinase	215	35	37.2	601	2	T11677	probable transcript
143	36	38.3	997	2	A87320	TonB-dependent rec	216	35	37.2	610	2	S95558	dynammin-like prote
144	36	38.3	1053	2	T30937	probable glycolipi	217	35	37.2	621	2	T15859	hypothetical prote
145	36	38.3	1118	2	S57833	transmembrane prot	218	35	37.2	655	2	S54183	acyl-CoA dehydroge
146	36	38.3	1206	2	T44376	DNA-directed RNA p	219	35	37.2	658	2	C75187	anaerobic ribonuc
147	36	38.3	1541	2	AC2474	heterocyst glycoli	220	35	37.2	681	2	T16353	hypothetical prote
148	36	38.3	1589	2	T13606	hypothetical prote	221	35	37.2	686	2	T06700	hypothetical prote
149	36	38.3	2021	2	AD2267	serine/threonine k	222	35	37.2	752	2	H90135	cell division cycl
150	36	38.3	2225	1	A23443	pyrimidine synthet	223	35	37.2	776	2	C83411	secretion protein
151	36	38.3	8243	2	T31307	type I fatty acid	224	35	37.2	780	2	E69095	carbon monoxide de
152	35.5	37.8	373	2	G69629	germination respon	225	35	37.2	787	2	G86436	hypothetical prote
153	35.5	37.8	373	2	B26470	spore germination	226	35	37.2	805	1	S19738	transitional endop
154	35.5	37.8	549	2	S04845	ig heavy chain pre	227	35	37.2	806	1	VPEG	transitional endop
155	35	37.2	45	2	PC1154	tumor rejection an	228	35	37.2	806	1	A55190	transitional endop
156	35	37.2	62	2	H84255	hypothetical prote	229	35	37.2	806	1	S25197	transitional endop
157	35	37.2	67	2	H97845	hypothetical prote	230	35	37.2	806	2	T02243	probable transitio
158	35	37.2	98	2	A28918	hypothetical prote	231	35	37.2	819	2	JC7240	two-pore calcium c
159	35	37.2	115	2	D81516	hypothetical prote	232	35	37.2	829	2	A33166	colorectal tumor s
160	35	37.2	116	2	E86633	hypothetical prote	233	35	37.2	906	2	T28034	hypothetical prote
161	35	37.2	177	2	T22603	hypothetical prote	234	35	37.2	912	2	G96830	hypothetical prote
162	35	37.2	185	2	H75168	2-ketoglutarate fe	235	35	37.2	952	2	T18900	disintegrin and me
163	35	37.2	185	2	D71046	probable ferredoxi	236	35	37.2	995	2	A88483	protein C05P11.1 [
164	35	37.2	199	2	F71462	hypothetical prote	237	35	37.2	1041	2	T15521	hypothetical prote
165	35	37.2	202	2	B61934	ferripyochelin bin	238	35	37.2	1095	1	A31225	phospholipase C (E
166	35	37.2	204	2	B69293	mercuric transport	239	35	37.2	1168	2	I56985	kalinin B1 - mouse
167	35	37.2	228	2	S26995	cellulose 1,4-beta	240	35	37.2	1459	2	G86457	unknown protein, 4
168	35	37.2	231	2	H75076	molybdenum formylm	241	35	37.2	1635	2	A10452	hemolysin importe
169	35	37.2	231	2	C97552	hypothetical prote	242	35	37.2	1713	2	A55347	adhesive ligand ep
170	35	37.2	231	2	AD2772	hypothetical prote	243	35	37.2	2049	2	T29227	hypothetical prote
171	35	37.2	235	2	G71658	hypothetical prote	244	35	37.2	2241	2	T20971	hypothetical prote
172	35	37.2	242	2	AB0719	probable percutiss	245	35	37.2	2242	2	A57541	pyrimidine synthet
173	35	37.2	249	2	T27782	hypothetical prote	246	35	37.2	2261	2	T20978	hypothetical prote
174	35	37.2	256	2	A81354	glutamine-binding	247	35	37.2	3591	1	S21010	filamentous hemagg
175	35	37.2	292	2	D98096	conserved hypothet	248	35	37.2	4644	1	A38905	dynein heavy chain

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105	41	43.6	476	1	ANGT_SHEEP	P20757	ovis aries	178	40	42.6	556	2	Q930H5_RHIME	Q930H5	rhizobium m
106	41	43.6	600	2	Q8YJX0_ANASP	Q8YJX0	anabaena sp	179	40	42.6	596	2	Q3GF99_9FIRM	Q3GF99	syntrophomo
107	41	43.6	627	2	Q4E2E3_TRYCR	Q4E2E3	trypanosoma	180	40	42.6	601	2	Q2LVLO_9DELT	Q2LVLO	syntrophus
108	41	43.6	643	2	Q8YSE2_ANASP	Q8YSE2	anabaena sp	181	40	42.6	617	1	CHIT_CAEEL	CHIT	caenorhabdi
109	41	43.6	728	2	Q8RG12_FUSNN	Q8RG12	fusobacteri	182	40	42.6	617	2	Q619N2_CABER	Q619N2	caenorhabdi
110	41	43.6	738	2	Q4CX81_TYCR	Q4CX81	trypanosoma	183	40	42.6	624	2	Q18448_CAEEL	Q18448	caenorhabdi
111	41	43.6	788	2	Q3M5K6_ANAVT	Q3M5K6	anabaena va	184	40	42.6	636	2	Q3Q9N8_GEOGM	Q3Q9N8	geobacter m
112	41	43.6	850	2	Q5SUC0_CRYNE	Q5SUC0	cryptococcu	185	40	42.6	686	2	Q2YBN8_NITMU	Q2YBN8	nitrosospir
113	41	43.6	850	2	Q5K125_CRYNE	Q5K125	cryptococcu	186	40	42.6	701	2	Q5U595_XENLA	Q5U595	xenopus lae
114	41	43.6	880	2	Q8PSG7_COREP	Q8PSG7	corynebacte	187	40	42.6	701	2	Q6NUB7_XENLA	Q6NUB7	xenopus lae
115	41	43.6	991	2	Q4IQ25_GIBZE	Q4IQ25	gibberella	188	40	42.6	738	2	Q3EDA9_ARATH	Q3EDA9	arabidopsis
116	41	43.6	996	2	Q39QNA_GEOGM	Q39QNA	geobacter m	189	40	42.6	910	2	Q8Q915_ADEG8	Q8Q915	avian adeno
117	41	43.6	996	2	Q8R2W5_MOUSE	Q8R2W5	mus musculus	190	40	42.6	970	2	Q875T3_SACCA	Q875T3	saccharomyc
118	41	43.6	1035	2	Q86TD1_HUMAN	Q86TD1	homo sapien	191	40	42.6	971	2	Q2SSN2_MYCCA	Q2SSN2	mycoplasma
119	41	43.6	1141	2	Q54Q43_DICDI	Q54Q43	dictyosteli	192	40	42.6	990	2	Q75C45_ASHGO	Q75C45	ashbya goss
120	41	43.6	1150	2	Q6D180_MOUSE	Q6D180	mus musculus	193	40	42.6	1007	2	Q4AS60_9BURK	Q4AS60	polaromonas
121	41	43.6	1236	2	Q387R5_9TRYP	Q387R5	trypanosoma	194	40	42.6	1048	2	Q8W517_IPOBA	Q8W517	ipomoea bat
122	41	43.6	1288	2	Q387R5_9TRYP	Q387R5	trypanosoma	195	40	42.6	1222	2	Q4RT35_TENG	Q4RT35	tetradodon n
123	41	43.6	1333	1	UTX_MOUSE	Q70546	mus musculus	196	40	42.6	1282	2	Q4QJ11_LEIMA	Q4QJ11	leishmania
124	41	43.6	1401	1	UTX_MOUSE	Q15550	homo sapien	197	40	42.6	1498	2	Q8CMR9_STAES	Q8CMR9	staphylococ
125	41	43.6	1401	2	Q52LL9_HUMAN	Q52LL9	homo sapien	198	40	42.6	1506	2	Q4L3C8_STAHL	Q4L3C8	staphylococ
126	41	43.6	1401	2	Q5JUV43_HUMAN	Q5JUV43	homo sapien	199	40	42.6	1510	2	Q9Z465_CORGL	Q9Z465	corynebacte
127	41	43.6	1406	2	Q59HG3_HUMAN	Q59HG3	homo sapien	200	40	42.6	1510	2	Q8NTW8_CORGL	Q8NTW8	corynebacte
128	41	43.6	1424	2	Q7TSG4_MOUSE	Q7TSG4	mus musculus	201	40	42.6	1522	2	Q2PYF9_9BACT	Q2PYF9	uncultured
129	41	43.6	1455	2	Q6AZS3_XENLA	Q6AZS3	xenopus lae	202	40	42.6	1751	2	Q92815_9RETR	Q92815	walleye der
130	41	43.6	2064	2	Q8B6R7_9RHAB	Q8B6R7	flanders vi	203	40	42.6	2531	2	Q8EGK0_SHEON	Q8EGK0	shewanella
131	41	43.6	2664	2	Q3P4K1_9GAMM	Q3P4K1	shewanella	204	40	42.6	2573	2	Q93CG8_PHOPR	Q93CG8	photobacter
132	41	43.6	2756	2	Q33904_9GAMM	Q33904	shewanella	205	40	42.6	2581	2	Q6LS55_PHOPR	Q6LS55	photobacter
133	41	43.6	3295	2	Q74RUS_YERPE	Q74RUS	yersinia pe	206	40	42.6	2619	2	Q3JTP3_9GAMM	Q3JTP3	shewanella
134	41	43.6	3295	2	Q8Z1A8_YERPE	Q8Z1A8	yersinia ps	207	40	42.6	2624	2	Q368M8_SHEWANA	Q368M8	shewanella
135	41	43.6	3378	2	Q66506_YERPS	Q66506	yersinia ps	208	40	42.6	2640	2	Q35ZQ6_9GAMM	Q35ZQ6	shewanella
136	40.5	43.1	254	2	Q5WMS2_LEGPL	Q5WMS2	legionella	209	40	42.6	2642	2	Q2ZRO9_SHEPU	Q2ZRO9	shewanella
137	40.5	43.1	254	2	Q3X5D2_LEGPA	Q3X5D2	legionella	210	40	42.6	2644	2	Q2X787_9GAMM	Q2X787	shewanella
138	40.5	43.1	254	2	Q3ZVW7_LEGPH	Q3ZVW7	legionella	211	40	42.6	2657	2	Q2Z774_9GAMM	Q2Z774	shewanella
139	40.5	43.1	332	2	Q8NN74_CORGL	Q8NN74	corynebacte	212	40	42.6	2693	2	Q3Q6R8_9GAMM	Q3Q6R8	shewanella
140	40.5	43.1	368	2	Q3FT34_9BURK	Q3FT34	rhodofera	213	40	42.6	4042	2	Q8KT64_PHOLU	Q8KT64	photorhabdu
141	40.5	43.1	483	2	Q30B58_ACTG3	Q30B58	acinetobact	214	39.5	42.0	203	1	RL18_PVRAB	RL18	pyrococcus
142	40.5	43.1	587	2	Q9NJX9_PLAGA	Q9NJX9	plasmodium	215	39.5	42.0	203	1	RL18_PVRHU	RL18	pyrococcus
143	40.5	43.1	891	2	Q36N24_MARHY	Q36N24	marinobacte	216	39.5	42.0	333	1	TRPD_PASMU	TRPD	pasteurella
144	40	42.6	87	2	Q3IKR8_PSEHT	Q3IKR8	pseudocalter	217	39.5	42.0	798	2	Q6ZC60_ORYSA	Q6ZC60	oryza sativ
145	40	42.6	209	2	Q48V17_STRPM	Q48V17	streptococc	218	39.5	42.0	847	2	Q2R0C6_ORYSA	Q2R0C6	oryza sativ
146	40	42.6	209	2	Q8K8H0_STRP3	Q8K8H0	streptococc	219	39.5	42.0	933	2	Q61WH7_homo sapien	Q61WH7	homo sapien
147	40	42.6	209	2	Q9A184_STRP1	Q9A184	streptococc	220	39.5	42.0	1288	2	Q54M67_DICDI	Q54M67	dictyosteli
148	40	42.6	213	2	Q8GVF4_ORYSA	Q8GVF4	oryza sativ	221	39.5	42.0	1811	2	Q36184_9VIRU	Q36184	plautia sta
149	40	42.6	219	2	Q2YZU2_9DELT	Q2YZU2	uncultured	222	39.5	42.0	2180	2	Q9VAS8_DROME	Q9VAS8	drosofila
150	40	42.6	230	2	Q3A158_SYNSC	Q3A158	synecococc	223	39.5	42.0	3966	2	Q7KVA7_DROME	Q7KVA7	drosofila
151	40	42.6	231	2	Q3A1G6_BACTN	Q3A1G6	bacteroides	224	39.5	42.0	36	2	Q700Q9_PIG	Q700Q9	sus scrofa
152	40	42.6	255	2	Q39CF2_BURS3	Q39CF2	burkholderi	225	39	41.5	36	2	Q8DVG1_STRMU	Q8DVG1	streptococc
153	40	42.6	275	2	Q7XL00_ORYSA	Q7XL00	oryza sativ	226	39	41.5	37	2	Q8DJA7_SYNEL	Q8DJA7	synecococc
154	40	42.6	292	2	Q3MH5_BOVIN	Q3MH5	bos taurus	227	39	41.5	78	2	Q3L1L3_SYNEL	Q3L1L3	synecococc
155	40	42.6	302	2	Q35N22_9BRAD	Q35N22	bradyrhizob	228	39	41.5	125	2	Q4ZW35_PSEU2	Q4ZW35	pseudomonas
156	40	42.6	311	2	Q3NDL6_9PROT	Q3NDL6	nitrosomona	229	39	41.5	131	2	Q9KU74_VIBCH	Q9KU74	vibrio chol
157	40	42.6	322	2	Q656F5_ORYSA	Q656F5	oryza sativ	230	39	41.5	139	2	Q3JJS4_METHU	Q3JJS4	methanospir
158	40	42.6	330	2	Q7PNF1_ANOGA	Q7PNF1	anopheles g	231	39	41.5	147	2	Q3G7H3_9DELT	Q3G7H3	pelobacter
159	40	42.6	331	2	Q4NLB8_9MICC	Q4NLB8	arthrobacte	232	39	41.5	152	2	Q5SP45_MOUSE	Q5SP45	mus musculu
160	40	42.6	334	2	Q30389_PSEAE	Q30389	pseudomonas	233	39	41.5	163	2	Q2SG77_9GAMM	Q2SG77	hahella che
161	40	42.6	334	2	Q3IE51_THICR	Q3IE51	thiomicrosp	234	39	41.5	171	2	Q9F8X4_TOHAC	Q9F8X4	nicotiana t
162	40	42.6	334	2	Q3RI15_FUSNN	Q3RI15	fusobacteri	235	39	41.5	184	2	Q5QX93_9LACO	Q5QX93	nitrosomona
163	40	42.6	353	2	Q4I5V6_GIBZE	Q4I5V6	gibberella	236	39	41.5	195	2	Q3N8G5_9PROT	Q3N8G5	9prot
164	40	42.6	368	2	Q98AB3_RHILO	Q98AB3	rhizobium l	237	39	41.5	205	2	Q6BVM3_DEBHA	Q6BVM3	debaromyce
165	40	42.6	372	2	Q3PHR7_PARDE	Q3PHR7	paracoccu	238	39	41.5	205	2	Q94306_BACFI	Q94306	bacillus fi
166	40	42.6	388	2	Q3FR59_9BURK	Q3FR59	rhodofera	239	39	41.5	208	2	Q8P2A4_STRP8	Q8P2A4	streptococc
167	40	42.6	394	2	Q5S1X0_IXOSC	Q5S1X0	ixodes scap	240	39	41.5	209	2	Q5XDL5_STRP6	Q5XDL5	streptococc
168	40	42.6	396	2	Q3MZK3_9DELT	Q3MZK3	syntrophoba	241	39	41.5	225	2	Q41QS9_FERAC	Q41QS9	ferroplasma
169	40	42.6	409	2	Q4Y9R3_TETNG	Q4Y9R3	tetradodon n	242	39	41.5	226	2	Q590H1_ATEGE	Q590H1	ateles geof
170	40	42.6	425	2	Q9YEU9_AERPE	Q9YEU9	aeropyrum p	243	39	41.5	226	2	Q5F0X4_PSEFL	Q5F0X4	pseudomonas
171	40	42.6	428	2	Q2JMU3_9CYAN	Q2JMU3	cyanobacter	244	39	41.5	227	2	Q54046_PSEAE	Q54046	pseudomonas
172	40	42.6	428	2	Q2JU94_9CYAN	Q2JU94	cyanobacter	245	39	41.5	231	2	Q3RV16_RALME	Q3RV16	ralstonia m
173	40	42.6	436	1	HMDH_ARCFU	Q28538	archaeoglob	246	39	41.5	239	2	Q65215_RAT	Q65215	rattus norv
174	40	42.6	477	2	Q3VCNO_MOUSE	Q3VCNO	mus musculus	247	39	41.5	246	2	Q7SCW1_NEUCR	Q7SCW1	neurospora
175	40	42.6	482	2	Q3UTR7_MOUSE	Q3UTR7	mus musculus	248	39	41.5	247	1	PYRF_CHRVO	PYRF	chromobacte
176	40	42.6	501	2	Q622M8_CABER	Q622M8	caenorhabdi	249	39	41.5	261	2	Q9G918_OCHDN	Q9G918	ochromonas
177	40	42.6	508	2	Q56V70_9ROSI	Q56V70	thecacaris	250	39	41.5					

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 9, 2006, 00:29:13 ; Search time 35.34 Seconds
(without alignments)
47.059 Million cell updates/sec

Title: US-10-797-626-2

Perfect score: 94

Sequence: 1 KGCSTQNAQLLSLVGKA 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

- 1: /EMC_Celerra_SID33/protdata/2/iaa/5 COMB.pep.*
- 2: /EMC_Celerra_SID33/protdata/2/iaa/6 COMB.pep.*
- 3: /EMC_Celerra_SID33/protdata/2/iaa/7 COMB.pep.*
- 4: /EMC_Celerra_SID33/protdata/2/iaa/H COMB.pep.*
- 5: /EMC_Celerra_SID33/protdata/2/iaa/PCUS COMB.pep.*
- 6: /EMC_Celerra_SID33/protdata/2/iaa/RE COMB.pep.*
- 7: /EMC_Celerra_SID33/protdata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	45	47.9	324	2	US-09-252-991A-29070
2	45	47.9	371	2	US-09-252-991A-29955
3	43	45.7	260	2	US-09-187-789-55
4	43	45.7	260	2	US-09-139-600-50
5	43	45.7	260	2	US-09-989-903-55
6	43	45.7	751	2	US-10-020-079-8
7	43	45.7	751	2	US-10-413-437-8
8	43	45.7	764	2	US-10-020-079-6
9	43	45.7	764	2	US-10-413-437-6
10	43	45.7	776	2	US-10-020-079-24
11	43	45.7	776	2	US-10-413-437-24
12	43	45.7	789	2	US-10-020-079-22
13	43	45.7	789	2	US-10-413-437-22
14	43	45.7	838	2	US-10-020-079-40
15	43	45.7	838	2	US-10-413-437-40
16	43	45.7	851	2	US-10-020-079-38
17	43	45.7	851	2	US-10-413-437-38
18	43	45.7	863	2	US-10-020-079-32
19	43	45.7	863	2	US-10-413-437-32
20	43	45.7	864	2	US-10-020-079-4
21	43	45.7	864	2	US-10-413-437-4
22	43	45.7	870	2	US-10-020-079-2
23	43	45.7	870	2	US-10-413-437-2
24	43	45.7	876	2	US-10-020-079-30
25	43	45.7	876	2	US-10-413-437-30
26	43	45.7	889	2	US-10-020-079-20

27	43	45.7	889	2	US-10-413-437-20	Sequence 20, Appl
28	43	45.7	895	2	US-10-020-079-18	Sequence 18, Appl
29	43	45.7	895	2	US-10-413-437-18	Sequence 18, Appl
30	43	45.7	951	2	US-10-020-079-36	Sequence 36, Appl
31	43	45.7	951	2	US-10-413-437-36	Sequence 36, Appl
32	43	45.7	957	2	US-10-020-079-34	Sequence 34, Appl
33	43	45.7	957	2	US-10-413-437-34	Sequence 34, Appl
34	43	45.7	976	2	US-10-020-079-28	Sequence 28, Appl
35	43	45.7	976	2	US-10-413-437-28	Sequence 28, Appl
36	43	45.7	982	2	US-10-020-079-26	Sequence 26, Appl
37	43	45.7	982	2	US-10-413-437-26	Sequence 26, Appl
38	42	44.7	719	1	US-07-943-843-4	Sequence 4, Appl
39	42	44.7	719	1	US-08-347-003-4	Sequence 4, Appl
40	41	43.6	1401	2	US-09-976-594-1035	Sequence 1035, Ap
41	41	43.6	2756	1	US-08-375-709-11	Sequence 11, Appl
42	41	43.6	2756	1	US-08-752-929-11	Sequence 11, Appl
43	41	43.6	2756	2	US-09-090-793-7	Sequence 7, Appl
44	41	43.6	2756	2	US-09-231-899-7	Sequence 7, Appl
45	40.5	43.1	332	2	US-09-602-787A-122	Sequence 122, App
46	40.5	43.1	587	2	US-09-579-383-4	Sequence 4, Appl
47	40	42.6	248	2	US-09-540-236-3589	Sequence 3589, Ap
48	40	42.6	563	2	US-09-252-991A-19387	Sequence 19387, A
49	40	42.6	645	2	US-09-710-279-2984	Sequence 2984, Ap
50	40	42.6	1501	2	US-09-710-279-2850	Sequence 2850, Ap
51	39	41.5	70	2	US-09-134-001C-3945	Sequence 10, Appl
52	39	41.5	297	2	US-09-289-346B-10	Sequence 4187, Ap
53	39	41.5	297	2	US-09-134-000C-4187	Sequence 4, Appl
54	39	41.5	376	1	US-08-464-148-4	Sequence 4, Appl
55	39	41.5	376	1	US-08-385-500-4	Sequence 4, Appl
56	39	41.5	376	1	US-08-846-784-4	Sequence 4, Appl
57	39	41.5	485	2	US-09-252-991A-20388	Sequence 20388, A
58	39	41.5	674	2	US-08-653-648A-14	Sequence 14, Appl
59	39	41.5	675	2	US-09-564-418-12	Sequence 12, Appl
60	39	41.5	842	2	US-09-248-796A-19371	Sequence 19371, A
61	39	41.5	1049	2	US-09-538-082-72	Sequence 72, Appl
62	39	41.5	1064	2	US-09-248-796A-16640	Sequence 16640, A
63	39	41.5	1456	2	US-09-976-594-168	Sequence 168, App
64	38.5	41.0	911	2	US-09-949-002-425	Sequence 425, App
65	38.5	41.0	1006	2	US-09-023-905A-12	Sequence 12, Appl
66	38.5	41.0	1006	2	US-09-949-002-361	Sequence 361, App
67	38	40.4	117	2	US-09-249-542-12	Sequence 12, Appl
68	38	40.4	174	2	US-09-270-767-32551	Sequence 32551, A
69	38	40.4	174	2	US-09-270-767-47768	Sequence 47768, A
70	38	40.4	240	2	US-09-252-991A-17600	Sequence 17600, A
71	38	40.4	380	2	US-09-248-796A-18198	Sequence 18198, A
72	38	40.4	412	2	US-09-248-796A-20552	Sequence 20552, A
73	38	40.4	441	2	US-09-950-071-2	Sequence 2, Appl
74	38	40.4	506	2	US-09-360-237-59	Sequence 59, Appl
75	38	40.4	519	2	US-09-270-767-36038	Sequence 36038, A
76	38	40.4	519	2	US-09-270-767-51255	Sequence 51255, A
77	38	40.4	1233	2	US-09-354-147C-7	Sequence 7, Appl
78	38	40.4	1243	2	US-09-354-147C-8	Sequence 8, Appl
79	38	40.4	1455	2	US-08-840-062-5	Sequence 5, Appl
80	38	40.4	1479	2	US-08-840-062-4	Sequence 4, Appl
81	38	40.4	1791	2	US-09-354-147C-42	Sequence 42, Appl
82	37	39.4	60	2	US-09-270-767-34098	Sequence 34098, A
83	37	39.4	60	2	US-09-270-767-49315	Sequence 49315, A
84	37	39.4	78	2	US-09-543-681A-5110	Sequence 5110, Ap
85	37	39.4	85	2	US-09-134-000C-6127	Sequence 6127, Ap
86	37	39.4	109	2	US-09-198-452A-11	Sequence 11, Appl
87	37	39.4	109	2	US-09-438-185A-2	Sequence 2, Appl
88	37	39.4	136	2	US-09-710-279-912	Sequence 912, App
89	37	39.4	154	2	US-09-489-039A-11527	Sequence 11527, A
90	37	39.4	180	2	US-09-134-000C-4611	Sequence 4611, Ap
91	37	39.4	248	2	US-09-482-273-126	Sequence 126, App
92	37	39.4	272	1	US-08-690-095-1	Sequence 1, Appl
93	37	39.4	272	2	US-09-113-789-1	Sequence 1, Appl
94	37	39.4	295	2	US-09-538-092-281	Sequence 281, App
95	37	39.4	318	2	US-09-489-039A-13257	Sequence 13257, A
96	37	39.4	329	2	US-09-710-279-2618	Sequence 2618, Ap
97	37	39.4	336	2	US-09-134-001C-5297	Sequence 5297, Ap
98	37	39.4	442	2	US-09-248-796A-26457	Sequence 26457, A
99	37	39.4	557	2	US-09-252-991A-22750	Sequence 22750, A

100	37	39.4	620	1	US-08-419-652-7	Sequence 7, Appli	173	35	37.2	292	2	US-09-583-110-3607	Sequence 3607, Ap
101	37	39.4	750	2	US-09-585-173B-12	Sequence 12, Appl	174	35	37.2	302	2	US-09-107-433-4911	Sequence 4911, Ap
102	37	39.4	984	2	US-09-171-461-14	Sequence 14, Appl	175	35	37.2	308	2	US-09-149-476-607	Sequence 607, App
103	37	39.4	984	2	US-09-970-711-14	Sequence 14, Appl	176	35	37.2	309	2	US-09-489-039A-12224	Sequence 12224, A
104	37	39.4	1001	1	US-07-797-556-6	Sequence 6, Appli	177	35	37.2	313	1	US-08-951-924A-2	Sequence 2, Appli
105	37	39.4	1001	1	US-07-943-843-2	Sequence 2, Appli	178	35	37.2	313	2	US-09-172-339-4	Sequence 4, Appli
106	37	39.4	1001	1	US-08-347-003-2	Sequence 2, Appli	179	35	37.2	313	2	US-09-420-211-11	Sequence 11, Appl
107	37	39.4	1049	2	US-09-107-532A-5966	Sequence 5966, Ap	180	35	37.2	318	2	US-09-270-767-44026	Sequence 44026, A
108	37	39.4	1067	2	US-09-107-532A-5148	Sequence 5148, Ap	181	35	37.2	348	2	US-09-270-767-44163	Sequence 44163, A
109	37	39.4	1079	2	US-09-058-489-22	Sequence 22, Appl	182	35	37.2	356	2	US-09-489-039A-9342	Sequence 9342, Ap
110	37	39.4	1097	1	US-07-943-843-6	Sequence 6, Appli	183	35	37.2	366	2	US-09-149-476-474	Sequence 474, App
111	37	39.4	1097	1	US-08-347-003-6	Sequence 6, Appli	184	35	37.2	399	2	US-09-248-796A-20092	Sequence 20092, A
112	37	39.4	1097	2	US-09-949-016-6209	Sequence 6209, Ap	185	35	37.2	407	2	US-09-962-955D-38	Sequence 38, Appl
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114	37	39.4	1119	3	US-09-907-155B-12	Sequence 12, Appl	187	35	37.2	429	2	US-09-770-509-26	Sequence 26, Appl
115	37	39.4	1240	2	US-09-058-489-23	Sequence 23, Appl	188	35	37.2	430	2	US-09-949-016-10102	Sequence 10102, A
116	37	39.4	1347	2	US-09-058-489-24	Sequence 24, Appl	189	35	37.2	441	2	US-09-149-476-372	Sequence 372, App
117	37	39.4	2158	2	US-10-144-198-34	Sequence 34, Appl	190	35	37.2	467	2	US-09-252-991A-23257	Sequence 23257, A
118	37	39.4	2265	2	US-10-144-198-35	Sequence 35, Appl	191	35	37.2	506	2	US-09-252-991A-24083	Sequence 24083, A
119	37	39.4	2697	2	US-10-144-198-12	Sequence 12, Appl	192	35	37.2	517	2	US-09-902-540-15771	Sequence 15771, A
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124	36.5	38.8	3174	1	US-08-477-451-3	Sequence 3, Appli	197	35	37.2	806	2	US-09-252-991A-16691	Sequence 16691, A
125	36	38.3	69	1	US-07-945-283-6	Sequence 6, Appli	198	35	37.2	818	2	US-09-252-991A-30225	Sequence 30225, A
126	36	38.3	128	2	US-09-270-767-40754	Sequence 40754, A	199	35	37.2	828	2	US-10-092-138A-26	Sequence 26, Appl
127	36	38.3	128	2	US-09-270-767-55970	Sequence 55970, A	200	35	37.2	828	2	US-08-681-219A-26	Sequence 26, Appl
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OM protein - protein search, using sw model

Run on: September 9, 2006, 00:32:28 ; Search time 19.76 Seconds
(without alignments)
67.548 Million cell updates/sec

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Perfect score: 94

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Total number of hits satisfying chosen parameters: 254368

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 1000 summaries

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Published Applications AA New:*

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- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	40	42.6	213	7	US-11-056-355B-62667
7	40	42.6	253	6	US-10-953-349-28899
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17	39	41.5	277	7	US-11-056-355B-51802
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51	38	40.4	1243	7	US-11-324-768-8	Sequence 8, Appl
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53	38	40.4	1791	7	US-11-313-450-18	Sequence 18, Appl
54	38	40.4	1791	7	US-11-324-768-42	Sequence 42, Appl
55	37	39.4	31	7	US-11-343-588-342	Sequence 342, App
56	37	39.4	103	7	US-11-293-697-4093	Sequence 4093, Ap
57	37	39.4	213	7	US-11-056-355B-7020	Sequence 7020, Ap
58	37	39.4	218	7	US-11-293-697-2853	Sequence 2853, Ap
59	37	39.4	255	7	US-11-056-355B-7019	Sequence 7019, Ap
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63	37	39.4	461	6	US-10-553-436-166	Sequence 166, App
64	37	39.4	542	6	US-10-449-902-54647	Sequence 54647, A
65	37	39.4	627	7	US-11-330-403-544	Sequence 544, App
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OM protein - protein search, using sw model

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61.619 Million cell updates/sec

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Perfect score: 85

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	44	51.8	148	AAG93238	Aag93238 C Glutami
5	44	51.8	204	ADN47346	Adn47346 Thermococ
6	43	50.6	13	ADS18077	Adsl8077 Laminin s
7	43	50.6	313	AAV34857	Aav34857 Chlamydia
8	41	48.2	127	AAB11673	Aab11673 A. vitis
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13	41	48.2	512	ADS25034	Ad25034 Bacterial
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22	41	48.2	2756	AAAB10467	Aab10467 Shewanell
23	41	48.2	2756	AAG64455	Aag64455 S. putref

24	40.5	47.6	696	7	ABO65887	AbO65887 Klebsiell
25	40	47.1	70	3	AAB40912	Ab40912 Human ORF
26	40	47.1	70	5	ABP08060	Abp08060 Human ORF
27	40	47.1	245	6	ABU43424	Abu43424 Protein e
28	40	47.1	337	4	ABB11797	Abb11797 Human sec
29	40	47.1	337	4	AAM79806	Aam79806 Human pro
30	40	47.1	358	8	ADN48113	Adn48113 Thermococ
31	40	47.1	371	7	ABO81209	AbO81209 Pseudomon
32	40	47.1	389	6	ABU42490	Abu42490 Protein e
33	40	47.1	397	4	AAU37106	Aau37106 Staphyloc
34	40	47.1	397	6	ABM73326	Abm73326 Staphyloc
35	40	47.1	652	7	ABM88164	Abm88164 Rice abio
36	40	47.1	1017	6	ABU42216	Abu42216 Protein e
37	40	47.1	1219	8	ADQ08796	Adq08796 Ciona int
38	40	47.1	1401	8	ADL13306	Adl13306 Human ste
39	40	47.1	1401	9	ADX07508	Adx07508 Cyclin-de
40	39.5	46.5	107	4	AAO09669	Aao09669 Human pol
41	39.5	46.5	452	5	ABB10110	Abb10110 Mouse cas
42	39.5	46.5	452	7	ADB79812	Adb79812 Rat caspa
43	39.5	46.5	2335	8	ADN19908	Adn19908 Bacterial
44	39.5	46.5	48	9	ABE16778	Abe16778 Hrib pept
45	39	45.9	227	6	ABU38639	Abu38639 Protein e
46	39	45.9	353	8	ADK69718	Adk69718 Rhizopus
47	39	45.9	357	8	ADK69725	Adk69725 Rhizopus
48	39	45.9	377	8	ADT59035	Adt59035 Plant pol
49	39	45.9	383	8	ADK69720	Adk69720 Rhizopus
50	39	45.9	485	7	ABO71642	AbO71642 Pseudomon
51	39	45.9	582	4	ABE63987	AbE63987 Drosophil
52	39	45.9	670	4	ABE60386	AbE60386 Drosophil
53	39	45.9	54	8	ADK47824	Adk47824 Streptoco
54	38	44.7	63	8	ADR96135	Adr96135 Novel S.
55	38	44.7	63	9	AEA60005	Aea60005 Streptoco
56	38	44.7	96	4	AAm23640	Aam23640 Human EST
57	38	44.7	131	6	ABU47148	Abu47148 Protein e
58	38	44.7	136	5	ABP28278	Abp28278 Streptoco
59	38	44.7	154	7	ABO65010	AbO65010 Klebsiell
60	38	44.7	174	8	ADX75550	Adx75550 Plant ful
61	38	44.7	203	4	AAE96735	Aae96735 Putative
62	38	44.7	246	8	ADX97068	Adx97068 Plant ful
63	38	44.7	274	6	ABU41181	Abu41181 Protein e
64	38	44.7	285	7	ADF06917	Adf06917 Bacterial
65	38	44.7	312	7	ABM90008	Abm90008 Rice abio
66	38	44.7	324	7	ABO80324	AbO80324 Pseudomon
67	38	44.7	438	8	ADJ49185	Adj49185 Oil-assoc
68	38	44.7	468	6	ABP79583	Abp79583 N. gonorr
69	38	44.7	550	7	ABO67452	AbO67452 Klebsiell
70	38	44.7	581	6	ABU37981	Abu37981 Protein e
71	38	44.7	635	4	ABB71475	Abb71475 Drosophil
72	38	44.7	645	4	AAG82945	Aag82945 S. epider
73	38	44.7	739	5	ABG80351	Abg80351 Clostridi
74	38	44.7	933	6	ABU43104	Abu43104 Protein e
75	38	44.7	1004	6	ABU29133	Abu29133 Protein e
76	38	44.7	1005	7	ADH88437	Adh88437 Enterococ
77	38	44.7	1501	4	AAG82878	Aag82878 S. epider
78	38	44.7	1529	5	ABG39100	Abg39100 Staphyloc
79	38	44.7	1529	8	ADS07312	AdS07312 Staphyloc
80	38	44.7	1778	4	ABE60081	AbE60081 Drosophil
81	38	44.7	1778	4	ABE60081	AbE60081 Drosophil
82	38	44.7	2015	4	ABE65890	AbE65890 Drosophil
83	38	44.7	2590	8	ADQ28932	AdQ28932 Mouse nov
84	37	43.5	19	4	AAm18519	Aam18519 Peptide #
85	37	43.5	19	4	ABB37558	Abb37558 Peptide #
86	37	43.5	19	4	AAm30979	Aam30979 Peptide #
87	37	43.5	19	4	ABB22850	Abb22850 Protein #
88	37	43.5	19	4	ABG52370	AbG52370 Human liv
89	37	43.5	49	7	ADD22433	Add22433 HLA-B46 T
90	37	43.5	49	7	ADI15929	Adi15929 Human pp
91	37	43.5	57	5	ABP07642	Abp07642 Human ORF
92	37	43.5	72	4	AAU44084	Aau44084 Propionib
93	37	43.5	72	6	ABM40603	Abm40603 Propionib
94	37	43.5	224	3	AAg20878	Aag20878 Arabidops
95	37	43.5	224	3	AAg50881	Aag50881 Arabidops
96	37	43.5	254	6	ABU33391	Abu33391 Protein e

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99	35	37.2	248	7	US-11-056-355B-98885	Sequence 98885, A	172	34	36.2	149	6	US-10-548-681-16	Sequence 16, Appl
100	35	37.2	248	7	US-11-056-355B-110124	Sequence 110124, A	173	34	36.2	157	6	US-10-953-349-9519	Sequence 9519, Ap
101	35	37.2	266	6	US-10-953-349-38275	Sequence 38275, A	174	34	36.2	161	6	US-10-953-349-9518	Sequence 9518, Ap
102	35	37.2	298	7	US-11-056-355B-10463	Sequence 10463, A	175	34	36.2	164	6	US-10-953-349-9517	Sequence 9517, Ap
103	35	37.2	300	6	US-10-196-749-452	Sequence 452, Ap	176	34	36.2	166	6	US-10-449-902-36481	Sequence 36481, A
104	35	37.2	300	6	US-10-953-349-6542	Sequence 6542, Ap	177	34	36.2	167	6	US-10-953-349-11904	Sequence 11904, A
105	35	37.2	300	7	US-11-056-355B-30774	Sequence 30774, A	178	34	36.2	172	6	US-10-449-902-50989	Sequence 50989, A
106	35	37.2	300	7	US-11-056-355B-34364	Sequence 34364, A	179	34	36.2	184	6	US-10-449-902-46746	Sequence 46746, A
107	35	37.2	300	7	US-11-056-355B-86775	Sequence 86775, A	180	34	36.2	210	7	US-11-056-355B-23604	Sequence 23604, A
108	35	37.2	300	7	US-11-056-355B-98884	Sequence 98884, A	181	34	36.2	235	7	US-11-056-355B-23603	Sequence 23603, A
109	35	37.2	300	7	US-11-056-355B-110123	Sequence 110123, A	182	34	36.2	240	6	US-10-953-349-35283	Sequence 35283, A
110	35	37.2	320	6	US-10-953-349-38274	Sequence 38274, A	183	34	36.2	247	7	US-11-056-355B-1215	Sequence 1215, Ap
111	35	37.2	319	6	US-10-449-902-43783	Sequence 43783, A	184	34	36.2	250	6	US-10-953-349-35282	Sequence 35282, A
112	35	37.2	330	7	US-11-056-355B-98883	Sequence 98883, A	185	34	36.2	250	6	US-11-330-403-11334	Sequence 11334, A
113	35	37.2	330	7	US-11-056-355B-110122	Sequence 110122, A	186	34	36.2	252	6	US-10-953-349-35281	Sequence 35281, A
114	35	37.2	333	6	US-10-953-349-6541	Sequence 6541, Ap	187	34	36.2	253	6	US-10-449-902-46405	Sequence 46405, A
115	35	37.2	333	7	US-11-056-355B-30773	Sequence 30773, A	188	34	36.2	261	6	US-10-953-349-33004	Sequence 33004, Ap
116	35	37.2	333	7	US-11-056-355B-34363	Sequence 34363, A	189	34	36.2	261	6	US-10-449-902-52646	Sequence 52646, A
117	35	37.2	333	7	US-11-056-355B-86774	Sequence 86774, A	190	34	36.2	261	7	US-11-056-355B-27812	Sequence 27812, A
118	35	37.2	343	6	US-10-449-902-29032	Sequence 29032, A	191	34	36.2	261	7	US-11-056-355B-31402	Sequence 31402, A
119	35	37.2	385	7	US-11-056-355B-97362	Sequence 97362, A	192	34	36.2	261	7	US-11-056-355B-85332	Sequence 85332, A
120	35	37.2	411	7	US-11-293-697-3582	Sequence 3582, Ap	193	34	36.2	274	7	US-11-293-697-3992	Sequence 3992, Ap
121	35	37.2	429	7	US-11-056-355B-37856	Sequence 37856, A	194	34	36.2	274	7	US-11-197-712-244	Sequence 244, App
122	35	37.2	429	7	US-11-056-355B-74917	Sequence 74917, A	195	34	36.2	279	6	US-10-953-349-3303	Sequence 3303, Ap
123	35	37.2	485	6	US-10-449-902-36775	Sequence 36775, A	196	34	36.2	279	6	US-11-056-355B-27811	Sequence 27811, A
124	35	37.2	489	6	US-10-953-349-511	Sequence 511, App	197	34	36.2	279	7	US-11-056-355B-31401	Sequence 31401, A
125	35	37.2	489	7	US-11-056-355B-35373	Sequence 35373, A	198	34	36.2	279	7	US-11-056-355B-85331	Sequence 85331, A
126	35	37.2	489	7	US-11-056-355B-103908	Sequence 103908, A	199	34	36.2	285	6	US-10-449-902-30527	Sequence 30527, A
127	35	37.2	489	7	US-11-056-355B-115147	Sequence 115147, A	200	34	36.2	295	6	US-10-449-902-48257	Sequence 48257, A
128	35	37.2	491	6	US-10-953-349-510	Sequence 510, App	201	34	36.2	296	6	US-10-505-928-137	Sequence 137, App
129	35	37.2	491	7	US-11-056-355B-35372	Sequence 35372, A	202	34	36.2	296	7	US-11-330-403-10819	Sequence 10819, A
130	35	37.2	491	7	US-11-056-355B-103907	Sequence 103907, A	203	34	36.2	296	7	US-11-330-403-11333	Sequence 11333, A
131	35	37.2	491	7	US-11-056-355B-115146	Sequence 115146, A	204	34	36.2	296	7	US-11-330-403-11336	Sequence 11336, A
132	35	37.2	511	7	US-11-056-355B-103906	Sequence 103906, A	205	34	36.2	296	7	US-11-330-403-11337	Sequence 11337, A
133	35	37.2	511	7	US-11-056-355B-115145	Sequence 115145, A	206	34	36.2	296	7	US-11-330-403-11342	Sequence 11342, A
134	35	37.2	512	6	US-10-953-349-19769	Sequence 19769, A	207	34	36.2	301	7	US-11-330-403-11311	Sequence 11311, A
135	35	37.2	512	6	US-11-056-355B-60366	Sequence 60366, A	208	34	36.2	302	6	US-11-056-355B-51197	Sequence 51197, A
136	35	37.2	513	6	US-10-953-349-509	Sequence 509, App	209	34	36.2	302	6	US-10-449-902-47806	Sequence 47806, A
137	35	37.2	513	7	US-11-056-355B-35371	Sequence 35371, A	210	34	36.2	303	6	US-10-953-349-3302	Sequence 3302, Ap
138	35	37.2	515	6	US-10-953-349-19768	Sequence 19768, A	211	34	36.2	303	7	US-11-056-355B-27810	Sequence 27810, A
139	35	37.2	515	6	US-11-056-355B-60365	Sequence 60365, A	212	34	36.2	303	7	US-11-056-355B-31400	Sequence 31400, A
140	35	37.2	523	6	US-10-953-349-19767	Sequence 19767, A	213	34	36.2	303	7	US-11-056-355B-85330	Sequence 85330, A
141	35	37.2	523	7	US-11-056-355B-60364	Sequence 60364, A	214	34	36.2	308	7	US-11-056-355B-23602	Sequence 23602, A
142	35	37.2	548	6	US-10-449-902-42290	Sequence 42290, A	215	34	36.2	309	6	US-10-449-902-47670	Sequence 47670, A
143	35	37.2	576	6	US-10-953-349-7006	Sequence 7006, Ap	216	34	36.2	323	6	US-10-449-902-33962	Sequence 33962, A
144	35	37.2	576	7	US-11-056-355B-21349	Sequence 21349, A	217	34	36.2	348	7	US-11-330-403-18131	Sequence 18131, A
145	35	37.2	610	7	US-11-056-355B-97587	Sequence 97587, A	218	34	36.2	382	6	US-10-449-902-52019	Sequence 52019, A
146	35	37.2	610	7	US-11-056-355B-108826	Sequence 108826, A	219	34	36.2	391	6	US-11-330-403-3407	Sequence 3407, Ap
147	35	37.2	610	7	US-11-056-355B-108826	Sequence 108826, A	220	34	36.2	395	6	US-10-449-902-55303	Sequence 55303, A
148	35	37.2	610	7	US-11-056-355B-109901	Sequence 109901, A	221	34	36.2	404	6	US-11-330-403-18376	Sequence 18376, A
149	35	37.2	764	6	US-10-449-902-45961	Sequence 45961, A	222	34	36.2	418	6	US-10-449-902-30915	Sequence 30915, A
150	35	37.2	806	7	US-11-134-228A-69	Sequence 69, Appl	223	34	36.2	418	6	US-10-449-902-48100	Sequence 48100, A
151	35	37.2	841	7	US-11-056-355B-107598	Sequence 107598, A	224	34	36.2	432	6	US-10-449-902-44328	Sequence 44328, A
152	35	37.2	841	7	US-11-056-355B-118837	Sequence 118837, A	225	34	36.2	432	6	US-11-056-355B-45730	Sequence 45730, A
153	35	37.2	844	7	US-11-056-355B-107597	Sequence 107597, A	226	34	36.2	432	6	US-10-449-902-52432	Sequence 52432, A
154	35	37.2	844	7	US-11-056-355B-118836	Sequence 118836, A	227	34	36.2	475	6	US-10-449-902-51200	Sequence 51200, A
155	35	37.2	853	7	US-11-056-355B-107596	Sequence 107596, A	228	34	36.2	489	6	US-10-953-349-5640	Sequence 5640, Ap
156	35	37.2	853	7	US-11-056-355B-118835	Sequence 118835, A	229	34	36.2	511	6	US-10-449-902-43807	Sequence 43807, A
157	35	37.2	995	6	US-10-528-563-8	Sequence 8, Appl1	230	34	36.2	517	7	US-11-056-355B-45729	Sequence 45729, A
158	35	37.2	1313	6	US-10-953-349-9733	Sequence 9733, Ap	231	34	36.2	528	7	US-11-056-355B-82342	Sequence 82342, A
159	35	37.2	1500	6	US-10-953-349-9732	Sequence 9732, Ap	232	34	36.2	531	6	US-10-449-902-43539	Sequence 43539, A
160	35	37.2	1511	6	US-10-953-349-9731	Sequence 9731, Ap	233	34	36.2	531	6	US-10-449-902-44583	Sequence 44583, A
161	35	37.2	2097	7	US-11-174-307B-148	Sequence 148, App	234	34	36.2	531	6	US-10-449-902-52432	Sequence 52432, A
162	35	37.2	2304	6	US-10-540-898-310	Sequence 310, App	235	34	36.2	531	6	US-10-449-902-52856	Sequence 52856, A
163	34.5	36.7	232	6	US-10-449-902-30620	Sequence 30620, A	236	34	36.2	532	7	US-11-056-355B-45728	Sequence 45728, A
164	34.5	36.7	232	6	US-10-449-902-55662	Sequence 55662, A	237	34	36.2	532	7	US-11-056-355B-82341	Sequence 82341, A
165	34.5	36.7	335	6	US-10-449-902-41619	Sequence 41619, A	238	34	36.2	609	7	US-11-056-355B-18353	Sequence 18353, A
166	34.5	36.7	350	6	US-10-449-902-51276	Sequence 51276, A	239	34	36.2	610	7	US-11-056-355B-66292	Sequence 66292, A
167	34.5	36.7	350	6	US-11-293-697-2801	Sequence 2801, Ap	240	34	36.2	627	7	US-11-056-355B-45857	Sequence 45857, A
168	34.5	36.7	561	7	US-11-330-403-558	Sequence 558, App	241	34	36.2	627	7	US-11-056-355B-72459	Sequence 72459, A
169	34	36.2	69	6	US-10-449-902-54631	Sequence 54631, A	242	34	36.2	627	7	US-11-330-403-278	Sequence 278, App
170	34	36.2	91	7	US-11-331-240-24	Sequence 24, Appl	243	34	36.2	628	6	US-10-449-902-52932	Sequence 52932, A
171	34	36.2	133	6	US-10-953-349-11905	Sequence 11905, A	244	34	36.2	642	7	US-11-056-355B-46723	Sequence 46723, A

97	37	43.5	254	9	ABP39665	Aeb39665	L. pneumo	170	36	42.4	164	5	ABP29430	Abp29430	Streptoco
98	37	43.5	261	9	ABP36245	Aeb36245	L. pneumo	171	36	42.4	170	8	ADV89055	Adv89055	Streptoco
99	37	43.5	263	3	AGS0880	Aeg50880	Arabidops	172	36	42.4	170	8	ADV80308	Adv80308	Streptoco
100	37	43.5	263	3	AGS20877	Aeg20877	Arabidops	173	36	42.4	173	4	AUA48434	Aua48434	Propionib
101	37	43.5	282	7	ADC95926	Adc95926	E. faeciu	174	36	42.4	173	6	ABM44953	Abm44953	Propionib
102	37	43.5	330	8	ADN47924	Adn47924	Thermococ	175	36	42.4	182	8	ADY23635	Ady23635	Plant ful
103	37	43.5	345	7	ADC23783	Adc23783	Protein s	176	36	42.4	200	8	ADV82426	Adv82426	Streptoco
104	37	43.5	345	8	ADH35884	Adh35884	Chemical	177	36	42.4	200	4	AAG91344	Aag91344	C glutami
105	37	43.5	345	8	ADG93585	Adg93585	Nitrilase	178	36	42.4	214	2	ABY34657	Aby34657	C. pneumo
106	37	43.5	345	8	ADI62182	Adi62182	Nitrilase	179	36	42.4	224	4	ABG08992	Abg08992	Novel hum
107	37	43.5	345	8	ADI64303	Adi64303	Nitrilase	180	36	42.4	240	7	ABO68854	AbO68854	Pseudomon
108	37	43.5	381	4	AAG89795	Aag89795	C glutami	181	36	42.4	243	6	ABM51048	Abm51048	Propionib
109	37	43.5	388	2	AAW26740	Aaw26740	Staphyloc	182	36	42.4	243	6	ABM51048	Abm51048	Propionib
110	37	43.5	400	6	ABM68527	Abm68527	Photorhab	183	36	42.4	247	8	ADK94323	Adk94323	Plant ful
111	37	43.5	431	4	ABM79671	Abm79671	Corynebac	184	36	42.4	257	7	ABO78861	AbO78861	Pseudomon
112	37	43.5	441	5	AAO17874	Aao17874	C glutami	185	36	42.4	263	8	ADY08521	Ady08521	Plant ful
113	37	43.5	441	9	AEC56408	Aec56408	Corynebac	186	36	42.4	272	4	ABG92867	Abg92867	C glutami
114	37	43.5	477	8	ADY09358	Ady09358	Plant ful	187	36	42.4	274	4	ABY79597	AbY79597	Corynebac
115	37	43.5	518	9	ADW18497	Adw18497	Pinus rad	188	36	42.4	276	5	ABM89125	Abm89125	Human pol
116	37	43.5	534	4	ABM63970	Abm63970	Drosophil	189	36	42.4	276	8	ADY22862	Ady22862	Plant ful
117	37	43.5	547	5	ABM91886	Abm91886	Herbicida	190	36	42.4	278	6	ABU25195	Abu25195	Protein e
118	37	43.5	548	4	ABM63196	Abm63196	Drosophil	191	36	42.4	285	7	ABU77335	Abu77335	Pseudomon
119	37	43.5	553	8	ADG74149	Adg74149	Rat prost	192	36	42.4	289	4	ABM80029	Abm80029	Corynebac
120	37	43.5	559	7	ADMO4660	Adm04660	Human pro	193	36	42.4	289	4	ABY79596	AbY79596	Corynebac
121	37	43.5	559	7	ADMO4658	Adm04658	Human pro	194	36	42.4	289	7	ADD13551	Add13551	C. glutam
122	37	43.5	559	9	AEC87590	Aec87590	Human CDN	195	36	42.4	289	7	ADD13707	Add13707	C. glutam
123	37	43.5	559	4	AEC87588	Aec87588	Human CDN	196	36	42.4	289	7	ADD13405	Add13405	C. glutam
124	37	43.5	560	4	AAG67397	Aag67397	Amino aci	197	36	42.4	289	9	AEC56314	Aec56314	Corynebac
125	37	43.5	613	2	AAW60593	Aaw60593	Cladospor	198	36	42.4	290	7	ADF06696	Adf06696	Bacterial
126	37	43.5	665	5	ABP65389	Abp65389	Bifidobac	199	36	42.4	297	7	ADH86302	Adh86302	Enterococ
127	37	43.5	868	4	ABG24427	Abg24427	Novel hum	200	36	42.4	313	4	AAQ73586	Aaq73586	Human col
128	37	43.5	886	8	ADS24527	Ads24527	Bacterial	201	36	42.4	341	2	AAQ91515	Aaq91515	Listeria
129	37	43.5	886	8	ADS29177	Ads29177	Bacterial	202	36	42.4	348	7	ADH87511	Adh87511	Enterococ
130	37	43.5	896	7	ADF05154	Adf05154	Bacterial	203	36	42.4	355	7	ADB65402	AdB65402	Human pro
131	37	43.5	1079	2	AAW81504	Aaw81504	Short for	204	36	42.4	394	7	ADC95557	AdC95557	E. faeciu
132	37	43.5	1240	2	AAW81505	Aaw81505	Medium fo	205	36	42.4	413	3	AAQ42399	Aaq42399	Arabidops
133	37	43.5	1347	2	AAW81506	Aaw81506	Long form	206	36	42.4	425	4	AAU59756	Aau59756	Propionib
134	37	43.5	1450	6	ADA89491	Ada89491	Staphyloc	207	36	42.4	428	6	ABM56275	Abm56275	Propionib
135	37	43.5	1491	4	AAU34072	Aau34072	Staphyloc	208	36	42.4	428	6	ABU33541	Abu33541	Protein e
136	37	43.5	1499	6	ABU16457	Abu16457	Protein e	209	36	42.4	431	6	ABU49807	Abu49807	Protein e
137	37	43.5	1502	4	AAU36569	Aau36569	Staphyloc	210	36	42.4	432	4	AAU34681	Aau34681	E. coli c
138	37	43.5	1502	6	ABM71608	Abm71608	Staphyloc	211	36	42.4	432	4	AAU38273	Aau38273	Salmonell
139	37	43.5	1509	6	ABU43942	Abu43942	Protein e	212	36	42.4	432	6	ABU27856	Abu27856	Protein e
140	37	43.5	1510	2	AAV01312	Aav01312	Glutamine	213	36	42.4	432	6	ABU48163	Abu48163	Protein e
141	37	43.5	1510	4	ABM79669	Abm79669	Corynebac	214	36	42.4	432	6	ABU28736	Abu28736	Protein e
142	37	43.5	1510	4	AAQ89953	Aaq89953	C glutami	215	36	42.4	432	6	ABU45604	Abu45604	Protein e
143	37	43.5	1510	7	ADD13595	Add13595	C glutami	216	36	42.4	432	6	ABU32200	Abu32200	Protein e
144	37	43.5	1560	1	AAQ94145	Aaq94145	S. cremor	217	36	42.4	432	8	ADS45097	AdS45097	Bacterial
145	37	43.5	1959	2	AAQ10562	Aaq10562	Mutant pr	218	36	42.4	432	9	ABE14273	Aeb14273	E. coli e
146	37	43.5	1962	2	AAQ10558	Aaq10558	Mutant pr	219	36	42.4	433	6	ABU39502	Abu39502	Protein e
147	37	43.5	1962	2	AAQ10559	Aaq10559	Mutant pr	220	36	42.4	433	6	ABU40605	Abu40605	Protein e
148	37	43.5	1962	2	AAQ10557	Aaq10557	Mutant pr	221	36	42.4	433	6	ABU49553	Abu49553	Protein e
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152	37	43.5	1968	2	AAQ10941	Aaq10941	Mutant pr	225	36	42.4	434	6	ABM70267	Abm70267	Photorhab
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154	37	43.5	2071	4	ABG17955	Abg17955	Novel hum	227	36	42.4	436	4	ABU30433	Abu30433	Protein e
155	37	43.5	2625	3	AAQ23832	Aaq23832	Shewanell	228	36	42.4	456	7	ADF05805	Adf05805	Bacterial
156	37	43.5	2652	4	AAQ78664	Aaq78664	Moritella	229	36	42.4	459	7	ABO63544	AbO63544	Klebsiell
157	37	43.5	2823	8	ADN22567	Adn22567	Bacterial	230	36	42.4	498	3	AAQ42398	Aaq42398	Arabidops
158	37	43.5	2823	8	ADN22568	Adn22568	Bacterial	231	36	42.4	506	7	ABM82744	Abm82744	Human pro
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OM protein - protein search, using sw model

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(without alignments)
74.233 Million cell updates/sec

Title: US-10-797-626-2

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Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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43	43	45.7	876	4	US-10-020-079-30	Sequence 30, Appl
44	43	45.7	876	4	US-10-413-437-30	Sequence 30, Appl
45	43	45.7	876	6	US-11-114-906-30	Sequence 30, Appl
46	43	45.7	889	4	US-10-020-079-20	Sequence 20, Appl
47	43	45.7	889	4	US-10-413-437-20	Sequence 20, Appl
48	43	45.7	889	6	US-11-114-906-20	Sequence 20, Appl
49	43	45.7	895	4	US-10-020-079-18	Sequence 18, Appl
50	43	45.7	895	4	US-10-413-437-18	Sequence 18, Appl
51	43	45.7	895	6	US-11-114-906-18	Sequence 18, Appl
52	43	45.7	951	4	US-10-020-079-36	Sequence 36, Appl
53	43	45.7	951	4	US-10-413-437-36	Sequence 36, Appl
54	43	45.7	951	6	US-11-114-906-36	Sequence 36, Appl
55	43	45.7	957	4	US-10-020-079-34	Sequence 34, Appl
56	43	45.7	957	4	US-10-413-437-34	Sequence 34, Appl
57	43	45.7	957	6	US-11-114-906-34	Sequence 34, Appl
58	43	45.7	976	4	US-10-020-079-28	Sequence 28, Appl
59	43	45.7	976	4	US-10-413-437-28	Sequence 28, Appl
60	43	45.7	976	6	US-11-114-906-28	Sequence 28, Appl
61	43	45.7	982	4	US-10-020-079-26	Sequence 26, Appl
62	43	45.7	982	4	US-10-413-437-26	Sequence 26, Appl
63	43	45.7	982	6	US-11-114-906-26	Sequence 26, Appl
64	43	45.7	1270	4	US-10-408-765A-2253	Sequence 2253, Ap
65	43	45.7	1308	5	US-10-840-512-166	Sequence 166, App
66	43	45.7	1321	4	US-10-271-507-2	Sequence 2, Appli
67	42	44.7	84	4	US-10-425-115-302810	Sequence 302810, A
68	42	44.7	313	5	US-10-450-763-39965	Sequence 39965, A
69	42	44.7	330	5	US-10-450-763-33143	Sequence 33143, A
70	41	43.6	154	5	US-10-450-763-54264	Sequence 54264, A
71	41	43.6	167	5	US-10-506-454-545	Sequence 545, App
72	41	43.6	263	4	US-10-813-805-22	Sequence 22, Appl
73	41	43.6	389	4	US-10-062-254-246	Sequence 246, App
74	41	43.6	396	4	US-10-425-115-223225	Sequence 223225, A
75	41	43.6	421	6	US-11-097-143-16236	Sequence 8220, Ap
76	41	43.6	428	6	US-11-097-143-8220	Sequence 45491, A
77	41	43.6	431	5	US-10-450-763-45491	Sequence 8914, Ap
78	41	43.6	728	5	US-10-732-923-8914	Sequence 7, Appli
79	41	43.6	1154	5	US-10-487-092-26	Sequence 26, Appl
80	41	43.6	254	4	US-10-331-061-7	Sequence 7, Appli
81	40.5	43.1	254	4	US-10-282-122A-61315	Sequence 61315, A
82	40.5	43.1	332	3	US-09-738-626-6060	Sequence 6060, App
83	40.5	43.1	332	4	US-10-627-476-122	Sequence 122, App
84	40	42.6	103	6	US-11-096-568A-13699	Sequence 13699, A
85	40	42.6	162	4	US-10-424-599-211289	Sequence 211289, A
86	40	42.6	173	6	US-11-096-568A-13697	Sequence 13697, A
87	40	42.6	175	4	US-10-425-115-296063	Sequence 296063, A
88	40	42.6	191	4	US-10-767-701-33820	Sequence 33820, A
89	40	42.6	253	4	US-10-437-963-196428	Sequence 196428, A
90	40	42.6	255	4	US-10-425-114-57823	Sequence 57823, A
91	40	42.6	275	4	US-10-437-963-114424	Sequence 114424, A
92	40	42.6	278	4	US-10-282-122A-53119	Sequence 53119, A
93	40	42.6	292	4	US-10-425-114-38434	Sequence 38434, A
94	40	42.6	431	6	US-11-055-822-76	Sequence 76, Appl
95	40	42.6	436	4	US-10-369-493-21378	Sequence 21378, A
96	40	42.6	436	4	US-10-041-018-235	Sequence 235, App
97	40	42.6	448	4	US-10-425-115-187601	Sequence 187601, A
98	40	42.6	477	4	US-10-425-114-50202	Sequence 50202, A
99	40	42.6	536	4	US-10-425-115-187602	Sequence 187602, A
100	40	42.6	617	4	US-10-369-493-6743	Sequence 6743, Ap

Best Available Copy

103	36	42.4	909	2	T06246	aspartate kinase (176	35	41.2	761	2	A81985	pilus secretin NMA
104	36	42.4	916	2	T06242	aspartate kinase (177	35	41.2	811	1	A40083	transcription fact
105	36	42.4	1053	2	T30937	probable glycolipi	178	35	41.2	829	2	A33166	colorectal tumor s
106	36	42.4	1118	2	S57833	transmembrane prot	179	35	41.2	862	2	S53913	FKH2 protein - yea
107	36	42.4	1206	2	T44376	DNA-directed RNA p	180	35	41.2	865	1	D70986	probable ABC trans
108	36	42.4	1258	2	T40737	probable calcium-t	181	35	41.2	871	2	A53429	acetylglutamate ki
109	36	42.4	1541	2	AG2474	heterocyst glycoli	182	35	41.2	907	2	H82261	hemolysin-related
110	36	42.4	1765	2	T42714	ankyrin 3, splice	183	35	41.2	952	2	A56678	hemauclein-alpha
111	36	42.4	1940	2	T42715	ankyrin 3, splice	184	35	41.2	1078	2	S48842	DNA-directed RNA p
112	36	42.4	1943	2	T42713	ankyrin 3, splice	185	35	41.2	1095	1	A31225	phospholipase C (E
113	36	42.4	1961	2	T42716	ankyrin 3, splice	186	35	41.2	1196	2	S35994	DNA repair protein
114	36	42.4	2167	2	S19444	hypothetical prote	187	35	41.2	1422	2	T18363	DNA-directed RNA p
115	36	42.4	2167	2	S19444	hypothetical prote	188	35	41.2	1469	2	H96622	probable ABC trans
116	36	42.4	2225	1	A23443	pyrimidine synthe	189	35	41.2	1469	2	H96622	peptidoglycan anch
117	36	42.4	4377	2	A55575	ankyrin 3, long sp	190	35	41.2	1530	2	AH1396	hypothetical prote
118	35.5	41.8	496	2	T19027	probable sterol O-	191	35	41.2	2054	2	T07584	conserved hypothet
119	35.5	41.8	614	2	A82832	protein-export mem	192	35	41.2	2155	2	AD2742	hypothetical prote
120	35	41.2	45	2	PC1154	tumor rejection an	193	35	41.2	2155	2	C75523	pyrimidine synthe
121	35	41.2	89	2	A87004	probable transcrip	194	35	41.2	2242	2	A57541	dynamin heavy chain
122	35	41.2	99	2	C64489	hypothetical prote	195	35	41.2	4644	1	A38905	hypothetical prote
123	35	41.2	116	2	E86633	hypothetical prote	196	34.5	40.6	177	2	T22603	hypothetical prote
124	35	41.2	127	2	G87731	protein W10C8.3 li	197	34.5	40.6	449	2	S76839	hypothetical prote
125	35	41.2	137	2	F95996	hypothetical prote	198	34.5	40.6	509	2	A13300	sugar transport AT
126	35	41.2	171	2	S20947	BTG1 protein - hum	199	34.5	40.6	605	2	AF1917	hypothetical prote
127	35	41.2	180	2	G71696	hypothetical prote	200	34	40.0	759	2	D84301	cell division cycl
128	35	41.2	184	2	B82307	16S rRNA processin	201	34	40.0	49	2	A82039	hypothetical prote
129	35	41.2	199	2	F71462	hypothetical prote	202	34	40.0	65	2	S02188	hypothetical prote
130	35	41.2	245	2	G87066	hypothetical prote	203	34	40.0	87	2	S33906	probable transcrip
131	35	41.2	247	2	T45250	glutamine-binding	204	34	40.0	87	2	S29614	regulatory protein
132	35	41.2	256	2	A81354	conserved hypotet	205	34	40.0	114	2	D86794	whiB protein - Str
133	35	41.2	269	2	B70124	UDP-3'-O-acetyl N-ace	206	34	40.0	125	2	T05633	hypothetical prote
134	35	41.2	282	2	F70452	xyloglucan endo-1,	207	34	40.0	138	2	AG1349	hypothetical prote
135	35	41.2	286	2	S71225	conserved hypotet	208	34	40.0	138	2	AB1720	hypothetical prote
136	35	41.2	292	2	D98096	conserved hypotet	209	34	40.0	144	2	S24805	hypothetical prote
137	35	41.2	292	2	B95232	conserved hypotet	210	34	40.0	148	2	AH0712	probable membrane
138	35	41.2	309	2	A80946	FdhE protein (impo	211	34	40.0	148	2	E64939	hypothetical prote
139	35	41.2	328	2	J00985	hydroxyproline-ric	212	34	40.0	172	2	AD0505	hypothetical prote
140	35	41.2	343	2	G71979	probable type II D	213	34	40.0	173	2	S18034	pathogenesis-relat
141	35	41.2	387	2	T27287	hypothetical prote	214	34	40.0	173	2	S18035	pathogenesis-relat
142	35	41.2	397	2	F90411	conserved hypotet	215	34	40.0	173	2	S18524	thiamatin-like pro
143	35	41.2	409	2	C82072	D-3-phosphoglycera	216	34	40.0	176	2	G91246	probable regulator
144	35	41.2	410	1	D8ECPG	phosphoglycerate d	217	34	40.0	190	2	S04355	somatotropin precu
145	35	41.2	410	2	AD0874	D-3-phosphoglycera	218	34	40.0	195	2	A53746	interferon, tropho
146	35	41.2	410	2	D85947	D-3-phosphoglycera	219	34	40.0	195	2	A61403	interferon alpha-I
147	35	41.2	410	2	H91101	D-3-phosphoglycera	220	34	40.0	195	2	I47070	interferon omega -
148	35	41.2	411	2	AF2320	hypothetical prote	221	34	40.0	195	2	C70899	probable guanylate
149	35	41.2	413	2	AC0112	phosphoglycerate d	222	34	40.0	208	2	D72046	hypothetical prote
150	35	41.2	423	2	B70931	probable PPG prote	223	34	40.0	221	2	T19468	conserved hypotet
151	35	41.2	430	2	I39727	mannopine biosynth	224	34	40.0	224	2	D72046	conserved hypotet
152	35	41.2	461	2	D95083	ABC transporter, A	225	34	40.0	224	2	A86579	CT668 hypothetical
153	35	41.2	461	2	H97950	hypothetical prote	226	34	40.0	238	2	T18788	hypothetical prote
154	35	41.2	473	2	B84143	Na+/H+ antiporter	227	34	40.0	241	2	D72751	hypothetical prote
155	35	41.2	476	1	JC2318	angiotensin precu	228	34	40.0	251	2	G69076	molibdopterin bios
156	35	41.2	486	2	C86645	Glu-tRNA amidotran	229	34	40.0	256	2	AE0511	FixA protein (impo
157	35	41.2	498	1	VH1VNA	nucleoprotein - in	230	34	40.0	257	2	F86540	CT254 hypothetical
158	35	41.2	510	2	S55204	hypothetical prote	231	34	40.0	257	2	G72081	conserved hypotet
159	35	41.2	528	2	S19366	hypothetical prote	232	34	40.0	261	2	AH2298	cobalt transport p
160	35	41.2	536	2	T23419	hypothetical prote	233	34	40.0	275	1	RSKT2	ribosomal protein
161	35	41.2	536	2	F85697	hypothetical prote	234	34	40.0	275	2	B75534	ribosomal protein
162	35	41.2	536	2	D64865	probable Na+/H+-ex	235	34	40.0	277	2	E75187	sugar abc transpor
163	35	41.2	536	2	F90839	hypothetical prote	236	34	40.0	277	2	D71220	probable sugar tra
164	35	41.2	538	2	A83018	probable sodium/hy	237	34	40.0	282	2	T50833	nematode resistanc
165	35	41.2	558	2	B48492	polysaccharide exp	238	34	40.0	290	2	B34585	arylamine N-acetyl
166	35	41.2	558	2	I41324	polysialic acid tr	239	34	40.0	292	2	A64592	methylenetetrahydr
167	35	41.2	565	1	C72550	methylmalonyl-CoA	240	34	40.0	292	2	T31325	menaquinone biosyn
168	35	41.2	575	2	C83198	probable acyl-CoA	241	34	40.0	299	2	S66007	yyak protein - Bac
169	35	41.2	577	2	A90723	probable Na+/H+ ex	242	34	40.0	317	2	A81402	probable ABC trans
170	35	41.2	578	2	B37852	phosphotransferase	243	34	40.0	319	2	A95316	annexin X - fruit
171	35	41.2	589	2	A82504	hypothetical prote	244	34	40.0	321	1	LUFF10	hypothetical prote
172	35	41.2	621	2	T15859	hypothetical prote	245	34	40.0	329	2	T32818	hypothetical prote
173	35	41.2	671	2	A65023	hypothetical prote	246	34	40.0	346	2	G83323	hypothetical prote
174	35	41.2	694	2	C83826	penicillin-binding	247	34	40.0	348	2	E82896	hemim permease U03
175	35	41.2	696	2	F83886	penicillin-binding	248	34	40.0	352	2	H71474	probable peptidogl

GenCore version 5.1.9

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OM protein - protein search, using sw model

Run on: September 9, 2006, 00:25:14 ; Search time 21.6 Seconds
(without alignments)
80.181 Million cell updates/sec

Title: US-10-797-626-3

Perfect score: 85

Sequence: 1 KGGSTQNAQLLSLVGKA 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 1000 summaries

Database :

FIR_80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	50.6	296	2	G86523
2	43	50.6	296	2	G72099
3	43	50.6	643	2	A2199
4	42	49.4	531	2	C97141
5	41	48.2	298	2	D71543
6	41	48.2	372	1	G70817
7	41	48.2	503	1	VMUT1B
8	41	48.2	2756	2	T30183
9	40	47.1	254	2	H69776
10	40	47.1	260	2	D75404
11	40	47.1	285	2	F84986
12	40	47.1	303	2	G64405
13	40	47.1	351	1	A55962
14	40	47.1	389	2	E90039
15	40	47.1	398	2	T44688
16	40	47.1	445	2	D69869
17	40	47.1	1401	2	T02255
18	39.5	46.5	452	2	JG6507
19	39.5	46.5	2335	2	T40186
20	39	45.9	55	2	B97548
21	39	45.9	139	2	D82296
22	39	45.9	227	2	D83162
23	39	45.9	298	2	C81696
24	39	45.9	326	2	AC2953
25	39	45.9	326	2	B98330
26	39	45.9	425	2	C72744
27	39	45.9	699	2	H87275
28	38.5	45.3	431	2	T16191
29	38	44.7	158	2	S75349

30	38	44.7	197	2	AB2571	hypothetical prote
31	38	44.7	203	2	E75145	1su ribosomal prot
32	38	44.7	206	2	A71185	probable ribosomal
33	38	44.7	292	2	T14627	hypothetical prote
34	38	44.7	317	2	G72342	L-isaspartate(D-a
35	38	44.7	330	2	E89899	protein C36C5.6 [i
36	38	44.7	375	2	C83884	arabinose operon t
37	38	44.7	581	2	B81909	exodeoxyribonuclea
38	38	44.7	850	2	AE1954	hypothetical prote
39	38	44.7	1168	2	I56985	kallinin B1 - mouse
40	38	44.7	1902	1	B44858	lactocepin (EC 3.4
41	38	44.7	2533	2	T28675	alpha-51D-immobili
42	38	44.7	2533	2	T28674	alpha-51D-immobili
43	38	44.7	2543	2	T31687	surface antigen - p
44	37.5	44.1	437	2	AF0667	probable phosphotr
45	37	43.5	76	2	AF2168	hypothetical prote
46	37	43.5	101	2	B75168	2-ketoglutarate fe
47	37	43.5	162	2	F81413	hypothetical prote
48	37	43.5	188	2	T52029	hypothetical prote
49	37	43.5	237	2	B84377	dTMP kinase (EC 2.
50	37	43.5	246	2	T00541	hypothetical prote
51	37	43.5	267	2	S72583	abc1 protein - Myc
52	37	43.5	349	1	JC5490	opsin, pineal glan
53	37	43.5	354	2	T36762	probable membrane
54	37	43.5	403	2	C70815	probable beta-reto
55	37	43.5	425	2	D88115	protein F53C3.11 l
56	37	43.5	446	2	D90238	aspartokinase (akH
57	37	43.5	457	2	S03961	ig mu chain C regi
58	37	43.5	473	2	A86989	conserved hypotet
59	37	43.5	547	2	T00977	probable pectinest
60	37	43.5	561	2	T11378	NADH2 dehydrogenas
61	37	43.5	702	2	JC7890	fructan beta-fruct
62	37	43.5	1217	2	F97177	alpha-glucosidase
63	37	43.5	1347	2	T02214	ubiquitous TPR mot
64	37	43.5	1451	2	B86286	F9L1.15 protein -
65	37	43.5	1499	2	A89813	glutamate synthase
66	37	43.5	1902	2	S06997	lactocepin (EC 3.4
67	37	43.5	1902	2	B45764	lactocepin (EC 3.4
68	37	43.5	1962	2	A32634	lactocepin (EC 3.4
69	37	43.5	2823	2	F87908	protein T22A3.8 [i
70	37	43.5	2823	2	T21064	hypothetical prote
71	37	43.5	3102	2	T43291	laminin alpha chai
72	36.5	42.9	513	2	AI2555	hypothetical prote
73	36	42.4	150	2	AH0371	probable membrane
74	36	42.4	227	2	E83288	probable ATP-bindi
75	36	42.4	310	2	T01869	hypothetical prote
76	36	42.4	323	2	AB1659	hypothetical prote
77	36	42.4	327	2	AB0888	hypothetical prote
78	36	42.4	341	2	S69802	N-acetylneuramoyl-L
79	36	42.4	351	2	D82891	conserved hypotet
80	36	42.4	384	2	D90547	oligopeptide ABC t
81	36	42.4	400	2	S76446	hypothetical prote
82	36	42.4	431	2	AB0410	phosphopyruvate hy
83	36	42.4	432	1	NOEC	phosphopyruvate hy
84	36	42.4	432	2	H85928	enolase [imported]
85	36	42.4	432	2	G91083	enolase [imported]
86	36	42.4	432	2	AC0859	enolase [imported]
87	36	42.4	433	2	E82076	enolase VC2447 [im
88	36	42.4	436	2	E64103	phosphopyruvate hy
89	36	42.4	447	2	C70951	hypothetical prote
90	36	42.4	466	2	T01898	hypothetical prote
91	36	42.4	480	2	H85112	hypothetical prote
92	36	42.4	502	2	AF3223	conserved hypotet
93	36	42.4	506	2	H82991	exopolysphatase
94	36	42.4	507	2	T50054	probable transport
95	36	42.4	533	2	A86433	T518.19 protein -
96	36	42.4	585	2	H83199	phosphotransferase
97	36	42.4	597	1	B55513	hoxX protein - Alc
98	36	42.4	601	2	T11677	probable transcrip
99	36	42.4	667	2	D96923	uncharacterized co
100	36	42.4	708	2	T43109	cytolysin B transp
101	36	42.4	780	2	AE0061	organic solvent to
102	36	42.4	841	2	T14398	S-receptor kinase

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OM protein - protein search, using sw model

Run on: September 9, 2006, 00:11:36 ; Search time 189.62 Seconds
(without alignments)
92.687 Million cell updates/sec

Title: US-10-797-626-2

Perfect score: 94

Sequence: 1 KGCSTONAQALLSLIVGKA 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : UniProt_7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	56.4	460	2 Q2W121	MAGSA
2	49	52.1	174	2 Q2S7G9	9GAMM
3	48	51.1	577	2 Q2W664	CLOBE
4	47	50.0	301	1 IAN4	MOUSE
5	47	50.0	301	2 Q4VBX0	MOUSE
6	47	50.0	301	2 Q549W4	MOUSE
7	47	50.0	370	1 SLDL	DICDI
8	46	48.9	99	2 Q2RMN8	RHORU
9	46	48.9	427	2 Q4WKC3	ASPFU
10	46	48.9	523	2 Q3ORZ0	9RHOB
11	46	48.9	684	2 Q4NHR6	9MCC
12	45	47.9	510	2 Q38CP5	9TRYF
13	44.5	47.3	82	2 Q225W6	9GAMM
14	44.5	47.3	82	2 Q35WU8	9GAMM
15	44.5	47.3	798	2 Q6ZD67	ORYSA
16	44	46.8	150	2 Q2L3N1	MICAE
17	44	46.8	165	2 Q87RY4	VIBPA
18	44	46.8	169	2 Q87J15	VIBPA
19	44	46.8	191	2 Q55T15	CRYNE
20	44	46.8	191	2 Q5KIV2	CRYNE
21	44	46.8	285	1 FOLD	BUCAI
22	44	46.8	294	2 Q423F6	DESHA
23	44	46.8	308	2 Q5AYR6	EMENI
24	44	46.8	357	2 Q8SUY1	ENCCU
25	44	46.8	801	2 Q20550	CAEEL
26	44	46.8	865	2 Q3RA20	VIBMA
27	44	46.8	2542	2 Q3QG44	9GAMM
28	43.5	46.3	341	2 Q5NR30	ZYMMO
29	43.5	46.3	606	2 Q52619	ORYSA
30	43	45.7	272	2 Q3QUH1	9RHOB
31	43	45.7	287	2 Q9H6N8	HUMAN

32	43	45.7	449	1	CSUP	DROME
33	43	45.7	452	1	CASF2	MOUSE
34	43	45.7	452	1	CASF2	RAT
35	43	45.7	463	2	Q750V4	ASHGO
36	43	45.7	621	2	Q6ZNH0	HUMAN
37	43	45.7	621	2	Q7NIC2	GLOVI
38	43	45.7	782	2	Q3URR7	MOUSE
39	43	45.7	790	2	Q02744	PNECA
40	43	45.7	813	2	Q5WHJ9	BACSK
41	43	45.7	819	2	Q3M6E0	ANAVT
42	43	45.7	883	2	Q8SRT2	ENCCU
43	43	45.7	1320	2	Q96JH2	HUMAN
44	43	45.7	1321	2	Q2L6C6	HUMAN
45	43	45.7	1414	2	Q5TCY1	HUMAN
46	43	45.7	1521	2	Q54X75	DICDI
47	43	45.7	2884	2	Q4SHN1	TETNG
48	42	44.7	71	1	NIFU	PRAAL
49	42	44.7	106	2	Q8R454	MESAU
50	42	44.7	121	2	Q44MI4	CHLLI
51	42	44.7	168	2	Q4XMH7	PLACH
52	42	44.7	183	2	Q54X41	DICDI
53	42	44.7	239	2	Q2PYA2	9BACT
54	42	44.7	268	2	Q3AIY2	PELCD
55	42	44.7	276	2	Q4ZVM9	PSEU2
56	42	44.7	294	2	Q4UCD1	THEAN
57	42	44.7	303	1	CD47	BOVIN
58	42	44.7	377	2	Q4U9E7	THEAN
59	42	44.7	424	2	Q3SZH5	BOVIN
60	42	44.7	508	2	Q56V71	9ROSI
61	42	44.7	515	2	Q56VA6	9ROSI
62	42	44.7	599	2	Q86PH5	CAEBR
63	42	44.7	675	2	Q8SV89	ENCCU
64	42	44.7	698	2	Q8QKX8	9PHYC
65	42	44.7	719	2	Q3UKU5	MOUSE
66	42	44.7	719	2	Q510Y2	MOUSE
67	42	44.7	733	2	Q7UJB6	RHOBA
68	42	44.7	852	2	Q37R76	SPHRA
69	42	44.7	852	2	Q4T128	TETNG
70	42	44.7	1092	1	LIFR	MOUSE
71	42	44.7	1092	1	Q3U234	MOUSE
72	42	44.7	1731	2	Q72TM8	LEPIC
73	42	44.7	1731	2	Q8FIM0	LEPIN
74	42	44.7	2122	2	Q41XZ0	DESHA
75	41.5	44.1	128	2	Q6LWM2	PHOPR
76	41.5	44.1	133	2	Q4APZ0	9CHLB
77	41.5	44.1	859	2	Q61FT5	MOUSE
78	41.5	44.1	860	2	Q61FT6	RAT
79	41	43.6	167	2	Q8TXW4	METKA
80	41	43.6	174	2	Q5KFD8	CRYNE
81	41	43.6	224	2	Q590H3	9PRIM
82	41	43.6	226	2	Q590I1	9PRIM
83	41	43.6	228	2	Q590H7	HUMAN
84	41	43.6	228	2	Q590H2	HYLLA
85	41	43.6	228	2	Q590H4	PREEN
86	41	43.6	228	2	Q590H5	LEORO
87	41	43.6	228	2	Q590H6	CHEME
88	41	43.6	228	2	Q590H8	PONPY
89	41	43.6	228	2	Q590H9	MATCA
90	41	43.6	228	2	Q590I0	ATGE
91	41	43.6	228	2	Q590I2	LEMCA
92	41	43.6	229	2	Q3G008	9DELT
93	41	43.6	230	2	Q84FK5	ENTAG
94	41	43.6	249	2	Q06170	YEAST
95	41	43.6	260	2	Q4CN69	TRYCR
96	41	43.6	263	1	ONCM	MOUSE
97	41	43.6	263	2	Q3UIY5	MOUSE
98	41	43.6	263	2	Q5SPX6	MOUSE
99	41	43.6	278	2	Q34X74	9GAMM
100	41	43.6	308	2	Q55Q86	CRYNE
101	41	43.6	350	2	Q61Z77	CAEBR
102	41	43.6	427	2	Q9VVQ2	DROME
103	41	43.6	428	1	TERM	DROME
104	41	43.6	428	2	Q541G1	DROME

Q9V3A4	drosophila
P29594	m caspase-2
F55215	rattus norv
Q750V4	ashbya goss
Q6ZNH0	homo sapien
Q7NIC2	gloeobacter
Q3URR7	mus musculus
Q02744	pneumocysti
Q5WHJ9	bacillus cl
Q3M6E0	anabaena va
Q8SRT2	encephalito
Q96JH2	homo sapien
Q2L6C6	homo sapien
Q5TCY1	homo sapien
Q54X75	dictyosteli
Q4SHN1	tetradon n
P46045	frankia aln
Q8R454	mesocricetu
Q44MI4	chlorobium
Q4XMH7	plasmodium
Q54X41	dictyosteli
Q2PYA2	uncultured
Q3AIY2	pelobacter
Q4ZVM9	pseudomonas
Q4UCD1	thelateria a
Q9N0K1	bos taurus
Q4U9E7	thelateria a
Q3SZH5	bos taurus
Q56V71	thecacoris
Q56VA6	antidesma a
Q60PH5	caenorhabdi
Q8SV89	encephalito
Q8QKX8	ectocarpus
Q3UKU5	mus musculus
Q510Y2	mus musculus
Q7UJB6	rhodospirill
Q37R76	novosphingo
Q4T128	tetradon n
P42703	mus musculus
Q3U234	mus musculus
Q72TM8	leptospora
Q8FIM0	leptospora
Q41XZ0	desulfitoba
Q6LWM2	photobacter
Q4APZ0	chlorobium
Q61FT5	mus musculus
Q61FT6	rattus norv
Q8TXW4	methanopyru
Q5KFD8	cryptococcu
Q590H3	colobus sp.
Q590I1	gorilla gor
Q590H7	homo sapien
Q590H2	hylobates l
Q590H4	presbytis e
Q590H5	leontopithe
Q590H6	cheirogaleu
Q590H8	pongo pygma
Q590H9	ataca fasc
Q590I0	ateles geof
Q590I2	lemur catta
Q3G008	pelobacter
Q84FK5	enterobacte
Q06170	saccharomyc
Q4CN69	trypanosoma
P53347	mus musculus
Q3UIY5	mus musculus
Q5SPX6	mus musculus
Q34X74	alkalilimni
Q55Q86	cryptococcu
Q61Z77	caenorhabdi
Q9VVQ2	drosophila
P11455	drosophila
Q541G1	drosophila

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 9, 2006, 00:11:36 ; Search time 179.64 Seconds
(without alignments)
92.687 Million cell updates/sec

Title: US-10-797-626-3

Perfect score: 85

Sequence: 1 KGGSTQNAQLLSLVGKA 18

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

UniProt_7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	58.8	174	2	Q257G9 habella che
2	46	54.1	99	2	Q2RMN8 RHORU
3	46	54.1	329	2	Q44LV6 CHLOROB
4	46	54.1	883	2	Q5SR72 ENCCU
5	45.5	53.5	698	2	Q8QKX8 PHYC
6	45	52.9	261	2	Q6G918 OCHDN
7	45	52.9	798	2	Q6ZD67 ORYSA
8	45	52.9	819	2	Q3M6E0 ANAVT
9	44	51.8	148	1	NRDI CORGL
10	44	51.8	201	1	RL18 PYRKO
11	44	51.8	260	2	Q4CN69 TRYCR
12	44	51.8	391	2	Q974X7 SULTO
13	44	51.8	627	2	Q4E2E3 TRYCR
14	44	51.8	2542	2	Q3QG44 GACMM
15	43	50.6	83	2	Q8EDD9 SHEON
16	43	50.6	296	2	Q9Z8S5 CHLPN
17	43	50.6	297	2	Q823A8 CHLCV
18	43	50.6	321	2	Q58G36 NEOP
19	43	50.6	321	2	Q58H36 NEOP
20	43	50.6	321	2	Q58H42 NEOP
21	43	50.6	331	2	Q58G21 NEOP
22	43	50.6	331	2	Q58G25 NEOP
23	43	50.6	331	2	Q58G26 NEOP
24	43	50.6	331	2	Q58H16 NEOP
25	43	50.6	331	2	Q58H17 NEOP
26	43	50.6	331	2	Q58H21 NEOP
27	43	50.6	331	2	Q58H31 NEOP
28	43	50.6	331	2	Q4NLB8 WICC
29	43	50.6	334	2	Q6TUE9 RAT
30	43	50.6	340	2	Q58H24 NEOP
31	43	50.6	340	2	Q58H44 NEOP

Q58gy8	ufeus conco	350	2	Q58GY8_9NEOP
Q58gz3	constra ru	350	2	Q58GZ3_9NEOP
Q58h01	rhizagrotis	350	2	Q58H01_9NEOP
Q58h02	properigea	350	2	Q58H02_9NEOP
Q58h03	caradrina s	350	2	Q58H03_9NEOP
Q58h06	homorthodes	350	2	Q58H06_9NEOP
Q58h07	lasionycta	350	2	Q58H07_9NEOP
Q58h08	polla detra	350	2	Q58H08_9NEOP
Q58h12	protogygia	350	2	Q58H12_9NEOP
Q58h18	euxoa tocoy	350	2	Q58H18_9NEOP
Q58h19	feltia jacu	350	2	Q58H19_9NEOP
Q58h23	xestia bica	350	2	Q58H23_9NEOP
Q58h50	neochera do	350	2	Q58H50_9NEOP
Q95Y98	pseudaletia	476	2	Q95Y98_PSESE
Q95Y99	mamestra br	476	2	Q95Y99_MAMBR
O8YSE2	anabaena sp	643	2	O8YSE2_ANASP
O5UC0	cryptococcu	850	2	O5UC0_CRYNE
O5KI25	cryptococcu	850	2	O5KI25_CRYNE
Q3GC24	syntrophomo	936	2	Q3GC24_9FIRM
Q5CZH9	homo sapien	1861	2	Q5CZH9_HUMAN
Q4IQT5	gibberella	991	2	Q4IQT5_GIBZE
O5AYR6	EMENI	308	2	O5AYR6_EMENI
O4TGT6	TETNG	349	2	O4TGT6_TETNG
Q4I5V6	tetraodon n	353	2	Q4I5V6_GIBZE
Q4SUT8	tetraodon n	356	2	Q4SUT8_TETNG
O4QES5	schistosoma	413	2	O4QES5_SCHMA
O56V71	thecacoris	508	2	O56V71_9ROSI
O56VA6	antidesma a	515	2	O56VA6_9ROSI
O97HQ2	clostridium	531	2	O97HQ2_CLOAB
O6CY85	kluveromyc*	553	1	FN51_KLUULA
Q4Z9F2	staphylococ	587	2	Q4Z9F2_9CAUD
O55dt6	dictyosteli	787	2	O55DT6_DICDI
O5YQ8	cryptococcu	872	2	O5YQ8_CRYNE
O5KG63	CRYNE	872	2	O5KG63_CRYNE
Q3VB26	9SPHN	292	2	Q3VB26_9SPHN
Q5L5X4	CHLAB	297	2	Q5L5X4_CHLAB
Q3KME1	chlamydophi	298	2	Q3KME1_CHLTA
O84223	CHLTR	298	2	O84223_CHLTR
Q7X222	9BACT	336	2	Q7X222_9BACT
O61Z77	CABBR	350	2	O61Z77_CABBR
O53916	MYCTU	372	2	O53916_MYCTU
VSAL1	TRYBB	503	1	VSAL1_TRYBB
Q3K7I3	PSEPF	512	2	Q3K7I3_PSEPF
Q3ADH2	CARH2	522	2	Q3ADH2_CARH2
O9FD21	ORYSA	523	2	O9FD21_ORYSA
Q2WM64	CLOBE	577	2	Q2WM64_CLOBE
O8ETK3	OCEIH	589	2	O8ETK3_OCEIH
Q8VJ24	MYCTU	591	2	Q8VJ24_MYCTU
Q7TZU2	MYCBO	591	2	Q7TZU2_MYCBO
Q7X188	ORYSA	633	2	Q7X188_ORYSA
Q43ZL5	SOLUS	638	2	Q43ZL5_SOLUS
Q3M5K6	ANAVT	848	2	Q3M5K6_ANAVT
Q39QM4	GEONG	996	2	Q39QM4_GEONG
RPOC_PSE14		1399	1	RPOC_PSE14
RPOC_PSE2		1399	1	RPOC_PSE2
Q3P4K1	9GAMM	2664	2	Q3P4K1_9GAMM
Q33904	9GAMM	2756	2	Q33904_9GAMM
Q4KJ19	PSEF5	3211	2	Q4KJ19_PSEF5
Q3OB58	ACIG3	483	2	Q3OB58_ACIG3
Q8MXH4	CAEEL	66	2	Q8MXH4_CAEEL
Q7G6Z3	ANOAG	201	2	Q7G6Z3_ANOAG
Q590H3	9PRIM	224	2	Q590H3_9PRIM
Q590H2	HYLLA	228	2	Q590H2_HYLLA
Q590H4	PREEN	228	2	Q590H4_PREEN
Q590H5	LEORO	228	2	Q590H5_LEORO
Q590H6	CHEME	228	2	Q590H6_CHEME
Q590H8	PONPY	228	2	Q590H8_PONPY
Q590H9	MACFA	228	2	Q590H9_MACFA
Q59010	ATEGE	228	2	Q59010_ATEGE

105	40	47.1	228	2	Q59012	lemur catta	Q59012	178	39.5	46.5	452	1	CASP2_RAT	P55215	rattus norv
106	40	47.1	254	2	P96655	bacillus su	P96655	179	39.5	46.5	2335	1	TOR1_SCHPO	O14356	schizosacch
107	40	47.1	260	2	Q9RUM9	deinococcus	Q9RUM9	180	39.5	46.5	3966	1	Q7KVA7_DROME	Q7KVA7	drosophila
108	40	47.1	285	1	FOLD_BUCAI	buchnera ap	P57557	181	39	45.9	55	2	Q8USA6_AGR5	Q8USA6	agrobacteri
109	40	47.1	285	2	Q8XHW1_CLOPE	clostridium	Q8XHW1	182	39	45.9	139	2	Q8KU74_VIBCH	Q8KU74	vibrio chol
110	40	47.1	286	2	Q4MMH9_BACCE	clostridium	Q4MMH9	183	39	45.9	144	2	Q8ZIQ5_PYRAE	Q8ZIQ5	pyrobaculum
111	40	47.1	286	2	Q63CM0_BACCZ	bacillus ce	Q63CM0	184	39	45.9	170	2	Q4C517_CROWT	Q4C517	crocosphaer
112	40	47.1	286	2	Q6HK25_BACHK	bacillus th	Q6HK25	185	39	45.9	189	2	Q3ZYJ7_DEHSC	Q3ZYJ7	dehalococco
113	40	47.1	286	2	Q81EN8_BACCR	bacillus ce	Q81EN8	186	39	45.9	198	2	Q8B990_SHEON	Q8B990	shewanella
114	40	47.1	286	2	Q81RV2_BACAN	bacillus an	Q81RV2	187	39	45.9	198	2	Q5QF97_9CRUS	Q5QF97	amblyops ab
115	40	47.1	286	2	Q739X4_BACCL	bacillus ce	Q739X4	188	39	45.9	213	2	Q8GVF4_ORISA	Q8GVF4	oryza sativ
116	40	47.1	289	2	Q4EVR3_BACTI	bacillus th	Q4EVR3	189	39	45.9	225	2	Q41QS9_FERAC	Q41QS9	ferroplasma
117	40	47.1	293	2	Q4VOK7_XANCB	xanthomonas	Q4VOK7	190	39	45.9	225	2	Q3XM71_9PROT	Q3XM71	magnetococc
118	40	47.1	293	2	Q8PEA8_XANCP	xanthomonas	Q8PEA8	191	39	45.9	226	2	Q590H1_ATEGE	Q590H1	ateles geof
119	40	47.1	303	1	MTRE_METJA	methanococc	Q58257	192	39	45.9	226	2	Q9FOX4_PSEFL	Q9FOX4	pseudomonas
120	40	47.1	318	2	Q7MAC8_WOLSU	wolinella s	Q7MAC8	193	39	45.9	227	2	Q54046_PSEAE	Q54046	pseudomonas
121	40	47.1	351	1	Q8SP_CHICK	gallus gall	P51475	194	39	45.9	232	2	Q7U5L5_SYNPK	Q7U5L5	synecococc
122	40	47.1	358	2	Q5JGK9_PYRKO	pyrococcus	Q5JGK9	195	39	45.9	251	2	Q5P7N8_AZOSE	Q5P7N8	azoaracus sp
123	40	47.1	378	2	Q964K2_DROBS	drosophila	Q964K2	196	39	45.9	268	2	Q3A1Y2_PELCD	Q3A1Y2	pelobacter
124	40	47.1	384	2	Q6KYT7_PICTO	picophilus	Q6KYT7	197	39	45.9	278	2	Q34X74_9GAMM	Q34X74	alkalilimni
125	40	47.1	385	2	Q4L805_STAHI	staphylococ	Q4L805	198	39	45.9	286	2	Q31TF1_SHIBS	Q31TF1	shigella bo
126	40	47.1	389	2	Q2YZ45_STAAB	staphylococ	Q2YZ45	199	39	45.9	286	2	Q3YUD5_SHISS	Q3YUD5	shigella so
127	40	47.1	389	2	Q6G6T3_STAAS	staphylococ	Q6G6T3	200	39	45.9	298	2	Q9PKH1_CHLMU	Q9PKH1	chlamydia m
128	40	47.1	389	2	Q7A3U8_STAAR	staphylococ	Q7A3U8	201	39	45.9	314	1	RT09_NEUCR	RT09	neurospora
129	40	47.1	389	2	Q7A3U8_STAAR	staphylococ	Q7A3U8	202	39	45.9	323	2	Q36TT7_MARHY	Q36TT7	marinobacte
130	40	47.1	389	2	Q8NV31_STAAM	staphylococ	Q8NV31	203	39	45.9	326	2	Q89QC5_BRAJA	Q89QC5	bradyrhizob
131	40	47.1	389	2	Q8NV31_STAAM	staphylococ	Q8NV31	204	39	45.9	326	2	Q8UAZ2_AGR5	Q8UAZ2	agrobacteri
132	40	47.1	389	2	Q8HDG7_STAAC	staphylococ	Q8HDG7	205	39	45.9	340	2	Q58H26_MICRAT	Q58H26	micrathetis
133	40	47.1	396	2	Q3MZK3_9DELT	syntrophoba	Q3MZK3	206	39	45.9	350	2	Q58H43_9NEOP	Q58H43	autographa
134	40	47.1	398	2	Q87694_BACME	bacillus me	Q87694	207	39	45.9	383	2	Q5W9U0_RHIOA	Q5W9U0	rhizopus or
135	40	47.1	409	2	Q4T9R3_TETNG	tetradon n	Q4T9R3	208	39	45.9	425	2	Q9YEU9_AERPE	Q9YEU9	aeropyrum p
136	40	47.1	419	2	Q4D193_TFYCR	trypanosoma	Q4D193	209	39	45.9	452	2	Q5V618_HALMA	Q5V618	haloarcula
137	40	47.1	419	2	Q4DNV8_TFYCR	trypanosoma	Q4DNV8	210	39	45.9	459	2	Q4WV68_ASPFU	Q4WV68	aspergillus
138	40	47.1	435	2	Q5AAL8_CANAL	candida alb	Q5AAL8	211	39	45.9	465	2	Q4B7K1_BURVI	Q4B7K1	burkholderi
139	40	47.1	445	1	YKVU_BACSU	bacillus su	Q5AAL8	212	39	45.9	467	2	Q7SX10_BRARE	Q7SX10	brachydanio
140	40	47.1	446	2	Q2SK37_9GAMM	haella che	Q2SK37	213	39	45.9	481	2	Q6SPX9_MANSM	Q6SPX9	mannheimia
141	40	47.1	475	2	Q5W6J8_ORISA	oryza sativ	Q5W6J8	214	39	45.9	508	2	Q4VNM2_HYMNOC	Q4VNM2	hymenocardi
142	40	47.1	501	2	Q622W8_CAEER	caenorhabdi	Q622W8	215	39	45.9	524	2	Q21LGO_BORAV	Q21LGO	bordetella
143	40	47.1	503	2	Q4DNV7_TFYCR	trypanosoma	Q4DNV7	216	39	45.9	529	2	Q21696_CAEEL	Q21696	caenorhabdi
144	40	47.1	503	2	Q5PK9_TFYCR	trypanosoma	Q5PK9	217	39	45.9	582	2	Q9V4W9_DROME	Q9V4W9	drosophila
145	40	47.1	508	2	Q56V70_9ROSI	theacoris	Q56V70	218	39	45.9	617	2	Q2W986_MAGSA	Q2W986	magnetospir
146	40	47.1	588	2	Q4D192_TFYCR	trypanosoma	Q4D192	219	39	45.9	619	1	EX070_KLUJA	EX070	kluyveromyc
147	40	47.1	608	2	Q4NIP7_9MICO	arthrobacte	Q4NIP7	220	39	45.9	619	2	Q617F9_CAEER	Q617F9	caenorhabdi
148	40	47.1	611	2	Q2WPN6_CLOBE	clostridium	Q2WPN6	221	39	45.9	632	2	Q7XMF5_ORISA	Q7XMF5	oryza sativ
149	40	47.1	636	2	Q3ZL21_ESCBL	escherichia	Q3ZL21	222	39	45.9	641	2	Q8ZWQ5_PYRAE	Q8ZWQ5	pyrobaculum
150	40	47.1	670	2	Q8ZTL6_PYRAE	pyrobaculum	Q8ZTL6	223	39	45.9	670	2	Q9W474_DROME	Q9W474	drosophila
151	40	47.1	798	2	Q6ZC60_ORISA	oryza sativ	Q6ZC60	224	39	45.9	699	2	Q9ABL0_CAUCR	Q9ABL0	caulobacter
152	40	47.1	996	2	Q8R2W5_MOUSE	mus musculus	Q8R2W5	225	39	45.9	705	2	Q6AX28_XENLA	Q6AX28	xenopus lae
153	40	47.1	1007	2	Q4ASG0_9BURK	polaromonas	Q4ASG0	226	39	45.9	716	2	Q2PGX3_9PERC	Q2PGX3	takifugu ob
154	40	47.1	1025	2	Q4OSI8_DESAC	desulfuromo	Q4OSI8	227	39	45.9	721	2	Q4CSH4_TRYCR	Q4CSH4	trypanosoma
155	40	47.1	1035	2	Q86TD1_HUMAN	homo sapien	Q86TD1	228	39	45.9	721	2	Q4DDA0_TRYCR	Q4DDA0	trypanosoma
156	40	47.1	1150	2	Q6D180_MOUSE	mus musculus	Q6D180	229	39	45.9	810	2	Q3SEM6_PARTE	Q3SEM6	paramecium
157	40	47.1	1206	2	Q8ZXP1_PYRAE	pyrobaculum	Q8ZXP1	230	39	45.9	866	2	Q4SHZ0_TETNG	Q4SHZ0	tetradon n
158	40	47.1	1333	1	UTX_MOUSE	mus musculus	Q70546	231	39	45.9	1040	2	Q54U93_DICDI	Q54U93	dictyosteli
159	40	47.1	1401	1	UTX_HUMAN	homo sapien	Q15550	232	39	45.9	1112	2	Q8GD29_BORAV	Q8GD29	bordetella
160	40	47.1	1401	2	Q52L19_HUMAN	homo sapien	Q52L19	233	39	45.9	1219	2	Q21L04_BORAV	Q21L04	bordetella
161	40	47.1	1401	2	Q5JV43_HUMAN	homo sapien	Q5JV43	234	39	45.9	1239	2	Q3F8Z4_STRCO	Q3F8Z4	streptomyce
162	40	47.1	1406	2	Q59HG3_HUMAN	homo sapien	Q59HG3	235	39	45.9	1390	2	Q54U91_DICDI	Q54U91	dictyosteli
163	40	47.1	1424	2	Q7TSG4_MOUSE	mus musculus	Q7TSG4	236	39	45.9	1485	2	Q2R0G9_ORISA	Q2R0G9	oryza sativ
164	40	47.1	1455	2	Q6AZS3_XENLA	xenopus lae	Q6AZS3	237	39	45.9	1513	2	Q3ASQ1_CHICH	Q3ASQ1	chlorobium
165	40	47.1	2122	2	Q41XZ0_DESHA	desulfuromo	Q41XZ0	238	39	45.9	1943	2	Q4KXQ1_SCHMA	Q4KXQ1	schistosoma
166	40	47.1	2531	2	Q8EGK0_SHEON	shewanella	Q8EGK0	239	39	45.9	2620	2	Q3NUK2_SHEFLA	Q3NUK2	shewanella
167	40	47.1	2531	2	Q33CG8_PHOPR	photobacter	Q33CG8	240	39	45.9	3405	2	Q32ZD3_9FLAV	Q32ZD3	sepiik virus
168	40	47.1	2581	2	Q6LS55_PHOPR	photobacter	Q6LS55	241	39	45.9	4236	2	Q5U9X1_TETTH	Q5U9X1	tetrahymena
169	40	47.1	2619	2	Q33TF3_SHEWANEL	shewanella	Q33TF3	242	38.5	45.3	270	2	Q2N7F8_9RPHN	Q2N7F8	erythrobacte
170	40	47.1	2624	2	Q368M8_9GAMM	shewanella	Q368M8	243	38.5	45.3	272	2	Q3QUH1_9RHOA	Q3QUH1	silicibacte
171	40	47.1	2640	2	Q35Z06_9GAMM	shewanella	Q35Z06	244	38.5	45.3	341	2	Q5NR30_ZYMO	Q5NR30	zymomonas m
172	40	47.1	2642	2	Q22R09_SHEPU	shewanella	Q22R09	245	38.5	45.3	416	2	Q2WI29_CLOBE	Q2WI29	clostridium
173	40	47.1	2644	2	Q2X787_9GAMM	shewanella	Q2X787	246	38.5	45.3	513	2	Q19846_CAEEL	Q19846	caenorhabdi
174	40	47.1	2657	2	Q2Z774_9GAMM	shewanella	Q2Z774	247	38.5	45.3	513	2	Q612F1_CABER	Q612F1	caenorhabdi
175	40	47.1	2693	2	Q3Q6R8_9GAMM	shewanella	Q3Q6R8	248	38.5	45.3	515	2	Q5WRR6_CABER	Q5WRR6	caenorhabdi
176	40	47.1	6274	2	Q880E1_PSESM	pseudomonas	Q880E1	249	38.5	45.3	893	2	O12274_9DELA	O12274	simian t-ly
177	39.5	46.5	452	1	CASP2_MOUSE	caspace-2	P29594	250	38.5	45.3	893	2	Q6XQ04_9DELA	Q6XQ04	simian t-ly

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OM protein - protein search, using sw model

Run on: September 9, 2006, 00:29:13 ; Search time 33.48 Seconds
(without alignments)
47.059 Million cell updates/sec

Title: US-10-797-626-3

Perfect score: 85

Sequence: 1 KGGSTQNAQLLSLVGKA 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents_AA*

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- 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB pep.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	50.6	313	2	US-09-198-452A-275
2	43	50.6	321	2	US-09-438-185A-265
3	41	48.2	151	1	US-08-253-155A-44
4	41	48.2	2756	1	US-08-375-709-11
5	41	48.2	2756	1	US-08-752-929-11
6	41	48.2	2756	2	US-09-090-793-7
7	41	48.2	2756	2	US-09-231-899-7
8	40.5	47.6	696	2	US-09-489-039A-12404
9	40	47.1	201	2	US-09-248-796A-19314
10	40	47.1	371	2	US-09-252-991A-29955
11	40	47.1	1401	2	US-09-976-594-1035
12	39.5	46.5	260	2	US-09-187-789-55
13	39.5	46.5	260	2	US-09-139-600-50
14	39.5	46.5	260	2	US-09-989-903-55
15	39	45.9	485	2	US-09-252-991A-20388
16	38	44.7	54	2	US-09-583-110-4339
17	38	44.7	63	2	US-09-107-433-4770
18	38	44.7	154	2	US-09-489-039A-11527
19	38	44.7	285	2	US-09-543-681A-7202
20	38	44.7	324	2	US-09-252-991A-29070
21	38	44.7	550	2	US-09-489-039A-13969
22	38	44.7	645	2	US-09-710-279-2984
23	38	44.7	1005	2	US-09-134-000C-6322
24	38	44.7	1501	2	US-09-710-279-2850
25	38	44.7	1529	2	US-09-134-001C-3945
26	37	43.5	76	2	US-09-270-767-34207

27	37	43.5	76	2	US-09-270-767-49424	Sequence 49424, A
28	37	43.5	282	2	US-09-107-532A-5553	Sequence 5553, Ap
29	37	43.5	441	2	US-09-950-071-2	Sequence 2, Appl
30	37	43.5	612	1	US-08-746-283-31	Sequence 31, Appl
31	37	43.5	612	1	US-08-746-257A-29	Sequence 29, Appl
32	37	43.5	613	1	US-08-746-283-1	Sequence 1, Appl
33	37	43.5	613	1	US-08-746-283-3	Sequence 3, Appl
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35	37	43.5	613	1	US-08-746-257A-1	Sequence 1, Appl
36	37	43.5	613	1	US-09-347-878-48	Sequence 48, Appl
37	37	43.5	896	2	US-09-543-681A-5439	Sequence 5439, Ap
38	37	43.5	1079	2	US-09-058-489-22	Sequence 22, Appl
39	37	43.5	1240	2	US-09-058-489-23	Sequence 23, Appl
40	37	43.5	1347	2	US-09-058-489-24	Sequence 24, Appl
41	36.5	42.9	306	2	US-09-107-532A-5918	Sequence 5918, Ap
42	36.5	42.9	3174	1	US-08-477-451-3	Sequence 3, Appl
43	36	42.4	71	2	US-09-248-796A-23149	Sequence 23149, A
44	36	42.4	214	2	US-09-198-452A-75	Sequence 75, Appl
45	36	42.4	240	2	US-09-252-991A-17600	Sequence 17600, A
46	36	42.4	257	2	US-09-252-991A-27607	Sequence 27607, A
47	36	42.4	285	2	US-09-252-991A-26081	Sequence 26081, A
48	36	42.4	290	2	US-09-543-681A-6981	Sequence 6981, Ap
49	36	42.4	297	2	US-09-134-000C-4187	Sequence 4187, Ap
50	36	42.4	348	2	US-09-134-000C-5396	Sequence 5396, Ap
51	36	42.4	355	2	US-10-104-047-3556	Sequence 3556, Ap
52	36	42.4	394	2	US-09-107-532A-5184	Sequence 5184, Ap
53	36	42.4	456	2	US-09-543-681A-6090	Sequence 6090, Ap
54	36	42.4	459	2	US-09-489-039A-10061	Sequence 10061, A
55	36	42.4	506	2	US-09-949-016-7018	Sequence 7018, Ap
56	36	42.4	516	2	US-09-949-016-7989	Sequence 7989, Ap
57	36	42.4	557	2	US-09-252-991A-22750	Sequence 22750, A
58	36	42.4	657	2	US-09-543-681A-7109	Sequence 7109, Ap
59	36	42.4	771	2	US-09-634-238-229	Sequence 229, App
60	36	42.4	771	2	US-09-634-238-262	Sequence 262, App
61	36	42.4	780	2	US-09-785-381-11	Sequence 11, Appl
62	36	42.4	1088	2	US-09-082-059-2	Sequence 2, Appl
63	36	42.4	1287	2	US-09-252-991A-29606	Sequence 29606, A
64	36	42.4	1724	2	US-09-964-899-43	Sequence 43, Appl
65	36	42.4	3913	2	US-09-949-016-10933	Sequence 10933, A
66	36	42.4	4377	2	US-09-949-016-6978	Sequence 6978, Ap
67	35.5	41.8	496	2	US-09-326-203A-18	Sequence 18, Appl
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69	35	41.2	21	2	US-09-962-756-1649	Sequence 1649, Ap
70	35	41.2	85	2	US-09-270-767-59587	Sequence 59587, A
71	35	41.2	87	2	US-09-605-703B-1868	Sequence 1868, Ap
72	35	41.2	171	2	US-08-718-738-17	Sequence 17, Appl
73	35	41.2	171	2	US-09-221-844-17	Sequence 17, Appl
74	35	41.2	171	2	US-09-843-846-17	Sequence 8461, Ap
75	35	41.2	210	2	US-09-489-039A-8681	Sequence 59436, A
76	35	41.2	212	2	US-09-270-767-59436	Sequence 7387, Ap
77	35	41.2	221	2	US-09-949-016-7387	Sequence 6021, Ap
78	35	41.2	231	2	US-09-134-000C-6021	Sequence 279, App
79	35	41.2	248	2	US-09-634-238-279	Sequence 2, Appl
80	35	41.2	249	2	US-08-591-468-2	Sequence 38, Appl
81	35	41.2	249	2	US-09-650-324A-38	Sequence 38, Appl
82	35	41.2	249	2	US-10-039-112A-38	Sequence 2, Appl
83	35	41.2	249	5	PCT-US94-06430-2	Sequence 9, Appl
84	35	41.2	273	2	US-08-928-213B-9	Sequence 1920, Ap
85	35	41.2	276	2	US-09-605-703B-1920	Sequence 8919, Ap
86	35	41.2	288	2	US-09-489-039A-8919	Sequence 26, Appl
87	35	41.2	289	2	US-09-716-964B-26	Sequence 391, App
88	35	41.2	292	2	US-08-858-207A-391	Sequence 3607, Ap
89	35	41.2	292	2	US-09-583-110-3607	Sequence 4911, Ap
90	35	41.2	302	2	US-09-107-433-4911	Sequence 12224, A
91	35	41.2	309	2	US-09-489-039A-12224	Sequence 3534, Ap
92	35	41.2	312	2	US-09-134-001C-3534	Sequence 3104, Ap
93	35	41.2	312	2	US-09-710-279-3104	Sequence 21365, A
94	35	41.2	316	2	US-09-252-991A-21365	Sequence 44026, A
95	35	41.2	318	2	US-09-270-767-44026	Sequence 44163, A
96	35	41.2	348	2	US-09-270-767-44163	Sequence 2, Appl
97	35	41.2	375	2	US-09-444-412-2	Sequence 12, Appl
98	35	41.2	375	2	US-09-660-742-12	Sequence 36, Appl
99	35	41.2	375	2	US-09-825-414-36	

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100	35	41.2	375	2	US-09-825-414-62	Sequence 62, Appl	173	34	40.0	102	1	US-08-455-524B-26	Sequence 26, Appl
101	35	41.2	391	2	US-09-347-798-8	Sequence 8, Appl	174	34	40.0	102	1	US-08-455-021B-26	Sequence 26, Appl
102	35	41.2	410	2	US-08-411-760-14	Sequence 14, Appl	175	34	40.0	102	1	US-09-045-467-26	Sequence 26, Appl
103	35	41.2	412	2	US-09-540-236-3010	Sequence 3010, Ap	176	34	40.0	115	2	US-09-471-276-1439	Sequence 1439, Ap
104	35	41.2	415	2	US-09-347-798-10	Sequence 10, Appl	177	34	40.0	171	1	US-08-438-753B-30	Sequence 30, Appl
105	35	41.2	416	2	US-09-543-681A-5020	Sequence 5020, Ap	178	34	40.0	171	1	US-08-443-883A-30	Sequence 30, Appl
106	35	41.2	427	2	US-09-489-039A-12022	Sequence 12022, A	179	34	40.0	171	1	US-08-631-328-30	Sequence 30, Appl
107	35	41.2	454	2	US-09-716-964B-5	Sequence 5, Appl	180	34	40.0	171	1	US-08-455-524B-30	Sequence 30, Appl
108	35	41.2	461	2	US-09-583-110-2826	Sequence 2826, Ap	181	34	40.0	171	1	US-08-455-021B-30	Sequence 30, Appl
109	35	41.2	461	2	US-09-107-433-3936	Sequence 3936, Ap	182	34	40.0	171	2	US-09-045-467-30	Sequence 30, Appl
110	35	41.2	464	2	US-09-716-964B-4	Sequence 4, Appl	183	34	40.0	172	1	US-08-438-753B-4	Sequence 4, Appl
111	35	41.2	467	2	US-09-149-476-372	Sequence 372, Ap	184	34	40.0	172	1	US-08-438-753B-34	Sequence 34, Appl
112	35	41.2	486	2	US-09-107-532A-7212	Sequence 7212, Ap	185	34	40.0	172	1	US-08-438-753B-44	Sequence 44, Appl
113	35	41.2	495	2	US-09-252-981A-16768	Sequence 16768, A	186	34	40.0	172	1	US-08-443-883A-4	Sequence 4, Appl
114	35	41.2	498	2	US-09-270-767-45042	Sequence 45042, A	187	34	40.0	172	1	US-08-443-883A-34	Sequence 34, Appl
115	35	41.2	527	1	US-08-823-516-144	Sequence 144, App	188	34	40.0	172	1	US-08-443-883A-44	Sequence 44, Appl
116	35	41.2	527	2	US-09-940-244-144	Sequence 144, App	189	34	40.0	172	1	US-08-631-328-4	Sequence 4, Appl
117	35	41.2	527	2	US-09-381-212-144	Sequence 144, App	190	34	40.0	172	1	US-08-631-328-34	Sequence 34, Appl
118	35	41.2	527	2	US-09-713-601A-144	Sequence 144, App	191	34	40.0	172	1	US-08-631-328-44	Sequence 44, Appl
119	35	41.2	528	2	US-08-928-213B-8	Sequence 8, Appl	192	34	40.0	172	1	US-08-455-524B-4	Sequence 4, Appl
120	35	41.2	529	2	US-09-716-964B-2	Sequence 2, Appl	193	34	40.0	172	1	US-08-455-524B-34	Sequence 34, Appl
121	35	41.2	539	2	US-09-252-991A-22491	Sequence 22491, A	194	34	40.0	172	1	US-08-455-524B-44	Sequence 44, Appl
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124	35	41.2	597	2	US-09-252-991A-32657	Sequence 32657, A	197	34	40.0	172	1	US-08-455-021B-44	Sequence 44, Appl
125	35	41.2	749	2	US-09-562-737-96	Sequence 96, Appl	198	34	40.0	172	2	US-09-045-467-4	Sequence 4, Appl
126	35	41.2	769	2	US-09-701-271A-2	Sequence 2, Appl	199	34	40.0	172	2	US-09-045-467-34	Sequence 34, Appl
127	35	41.2	769	2	US-09-701-271A-4	Sequence 4, Appl	200	34	40.0	172	2	US-09-045-467-44	Sequence 44, Appl
128	35	41.2	769	2	US-09-701-271A-6	Sequence 6, Appl	201	34	40.0	172	2	US-08-616-904-4	Sequence 4, Appl
129	35	41.2	811	2	US-09-538-092-518	Sequence 518, App	202	34	40.0	172	2	US-08-616-904-6	Sequence 6, Appl
130	35	41.2	828	2	US-10-092-138A-26	Sequence 26, Appl	203	34	40.0	172	2	US-10-029-890-4	Sequence 4, Appl
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132	35	41.2	829	1	US-07-670-611-2	Sequence 2, Appl	205	34	40.0	194	2	US-09-487-792-5	Sequence 5, Appl
133	35	41.2	829	1	US-08-220-674-2	Sequence 2, Appl	206	34	40.0	194	2	US-09-908-594-5	Sequence 5, Appl
134	35	41.2	829	1	US-08-445-186-2	Sequence 2, Appl	207	34	40.0	195	1	US-08-438-753B-12	Sequence 12, Appl
135	35	41.2	829	1	US-08-446-549-2	Sequence 2, Appl	208	34	40.0	195	1	US-08-438-753B-32	Sequence 32, Appl
136	35	41.2	829	1	US-08-446-550-2	Sequence 2, Appl	209	34	40.0	195	1	US-08-443-883A-12	Sequence 12, Appl
137	35	41.2	955	1	US-08-500-857A-10	Sequence 10, Appl	210	34	40.0	195	1	US-08-443-883A-32	Sequence 32, Appl
138	35	41.2	983	2	US-09-538-092-1320	Sequence 1320, Ap	211	34	40.0	195	1	US-08-631-328-12	Sequence 12, Appl
139	35	41.2	1067	2	US-09-107-532A-5148	Sequence 5148, Ap	212	34	40.0	195	1	US-08-631-328-32	Sequence 32, Appl
140	34.5	40.6	114	2	US-09-134-000C-3879	Sequence 3879, Ap	213	34	40.0	195	1	US-08-455-524B-12	Sequence 12, Appl
141	34.5	40.6	200	2	US-09-717-364A-21	Sequence 21, Appl	214	34	40.0	195	1	US-08-455-524B-32	Sequence 32, Appl
142	34.5	40.6	513	2	US-09-248-796A-20548	Sequence 20548, A	215	34	40.0	195	1	US-08-455-021B-12	Sequence 12, Appl
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163	36	42.4	276	4	US-10-425-114-70646	Sequence 70646, A	236	36	42.4	780	5	US-10-631-467-1456	Sequence 1456, Ap
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173	36	42.4	355	4	US-10-104-047-3556	Sequence 3556, Ap	246	36	42.4	918	4	US-10-424-599-235347	Sequence 235347, A

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Perfect score: 85

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Searched: 254368 seqs, 70249769 residues

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Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	39	45.9	213	6	US-10-953-349-28900
8	39	45.9	213	7	US-11-056-355B-62667
9	39	45.9	216	6	US-10-953-349-30984
10	39	45.9	216	7	US-11-056-355B-62665
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83	35	41.2	302	7	US-11-056-355B-82887	Sequence 82887, A
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144	34	40.0	541	7	US-11-056-355B-87213	Sequence 87213, A	217	33	38.8	406	7	US-10-953-349-23104	Sequence 23104, A
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152	34	40.0	830	7	US-11-056-355B-24872	Sequence 24872, A	225	33	38.8	438	6	US-10-449-902-5402	Sequence 5402, A
153	34	40.0	1008	6	US-10-548-463-191	Sequence 191, App	226	33	38.8	438	7	US-11-330-403-6331	Sequence 6331, Ap
154	34	40.0	1224	6	US-10-506-630A-39	Sequence 39, Appl	227	33	38.8	440	7	US-11-056-355B-45011	Sequence 45011, A
155	33.5	39.4	106	7	US-11-347-179-155	Sequence 155, App	228	33	38.8	444	6	US-10-449-902-51332	Sequence 51332, A
156	33.5	39.4	644	6	US-10-449-902-48127	Sequence 48127, A	229	33	38.8	445	7	US-11-330-403-501	Sequence 501, App
157	33	38.8	91	7	US-11-331-240-24	Sequence 24, Appl	230	33	38.8	446	7	US-11-056-355B-2842	Sequence 2842, Ap
158	33	38.8	115	6	US-10-449-902-3764	Sequence 3764, A	231	33	38.8	451	7	US-11-247-138-2	Sequence 2, Appli
159	33	38.8	126	7	US-11-056-355B-59643	Sequence 59643, A	232	33	38.8	492	7	US-11-056-355B-45010	Sequence 45010, A
160	33	38.8	130	7	US-11-056-355B-24640	Sequence 24640, A	233	33	38.8	496	7	US-11-330-403-4732	Sequence 4732, Ap
161	33	38.8	130	7	US-11-056-355B-106670	Sequence 106670, A	234	33	38.8	501	7	US-11-056-355B-18298	Sequence 18298, A
162	33	38.8	130	7	US-11-056-355B-117909	Sequence 117909, A	235	33	38.8	501	7	US-11-056-355B-18297	Sequence 18297, A
163	33	38.8	132	7	US-11-056-355B-84501	Sequence 84501, A	236	33	38.8	510	7	US-11-056-355B-45009	Sequence 45009, A
164	33	38.8	135	7	US-11-056-355B-24639	Sequence 24639, A	237	33	38.8	515	6	US-10-953-349-11608	Sequence 11608, A
165	33	38.8	135	7	US-11-056-355B-106669	Sequence 106669, A	238	33	38.8	517	6	US-11-056-355B-47436	Sequence 47436, A
166	33	38.8	135	7	US-11-056-355B-117908	Sequence 117908, A	239	33	38.8	557	6	US-10-449-902-50128	Sequence 50128, A
167	33	38.8	136	7	US-11-330-403-10263	Sequence 10263, A	240	33	38.8	557	6	US-10-449-902-50128	Sequence 50128, A
168	33	38.8	137	7	US-11-056-355B-84500	Sequence 84500, A	241	33	38.8	591	6	US-10-953-349-11607	Sequence 11607, A
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